

FIGURE 1A

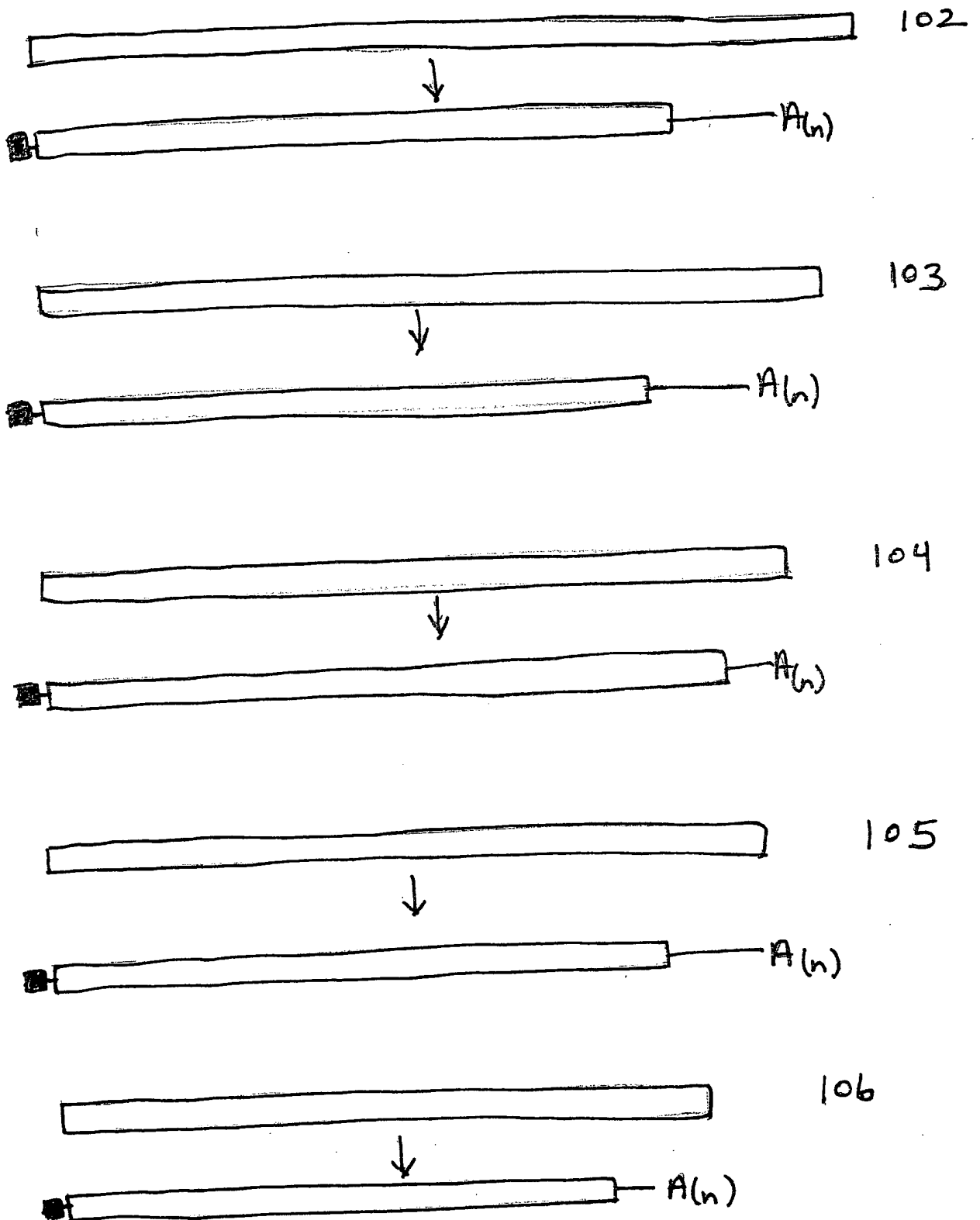


FIGURE 1B-1

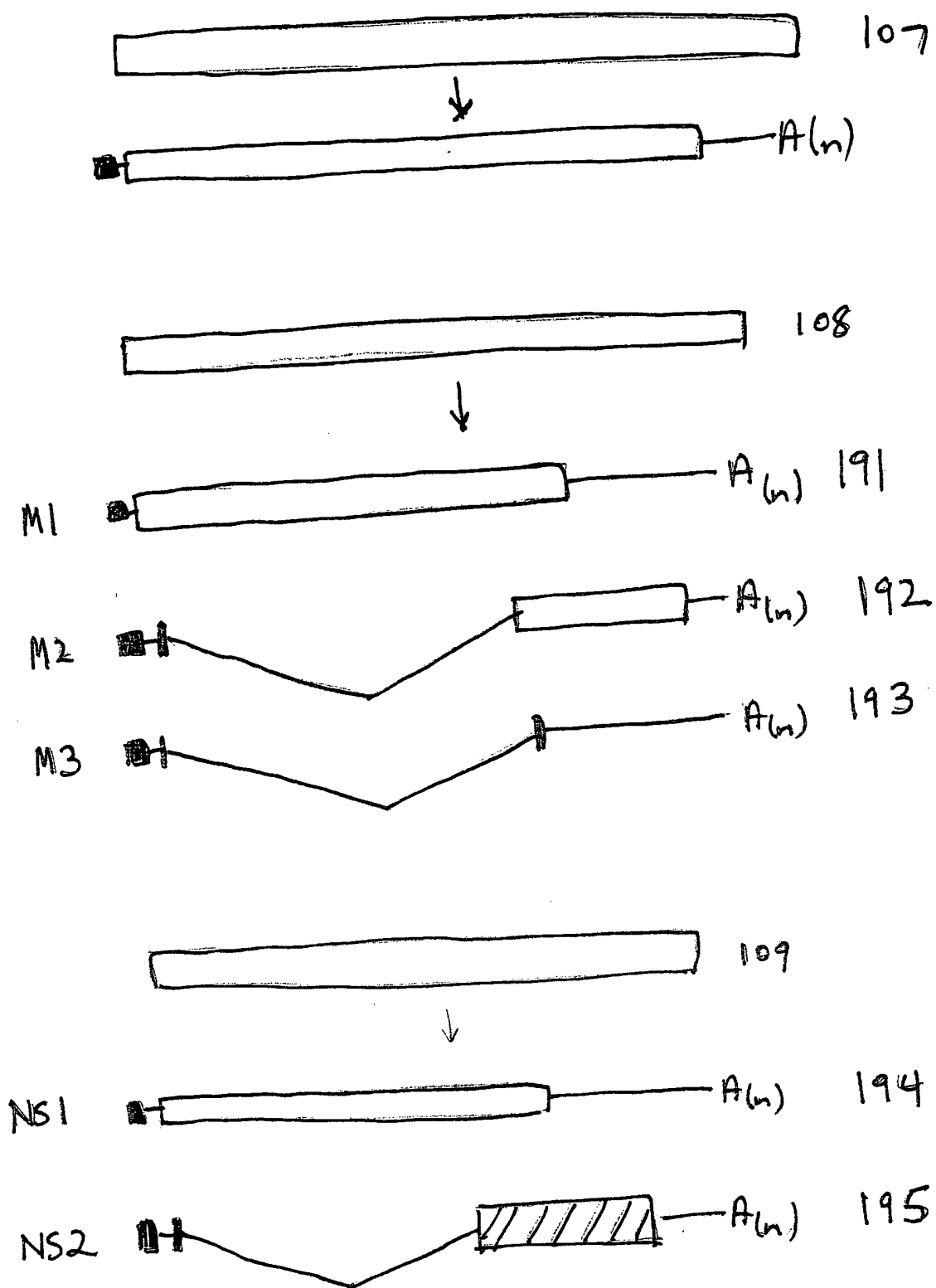


FIGURE 1B-2

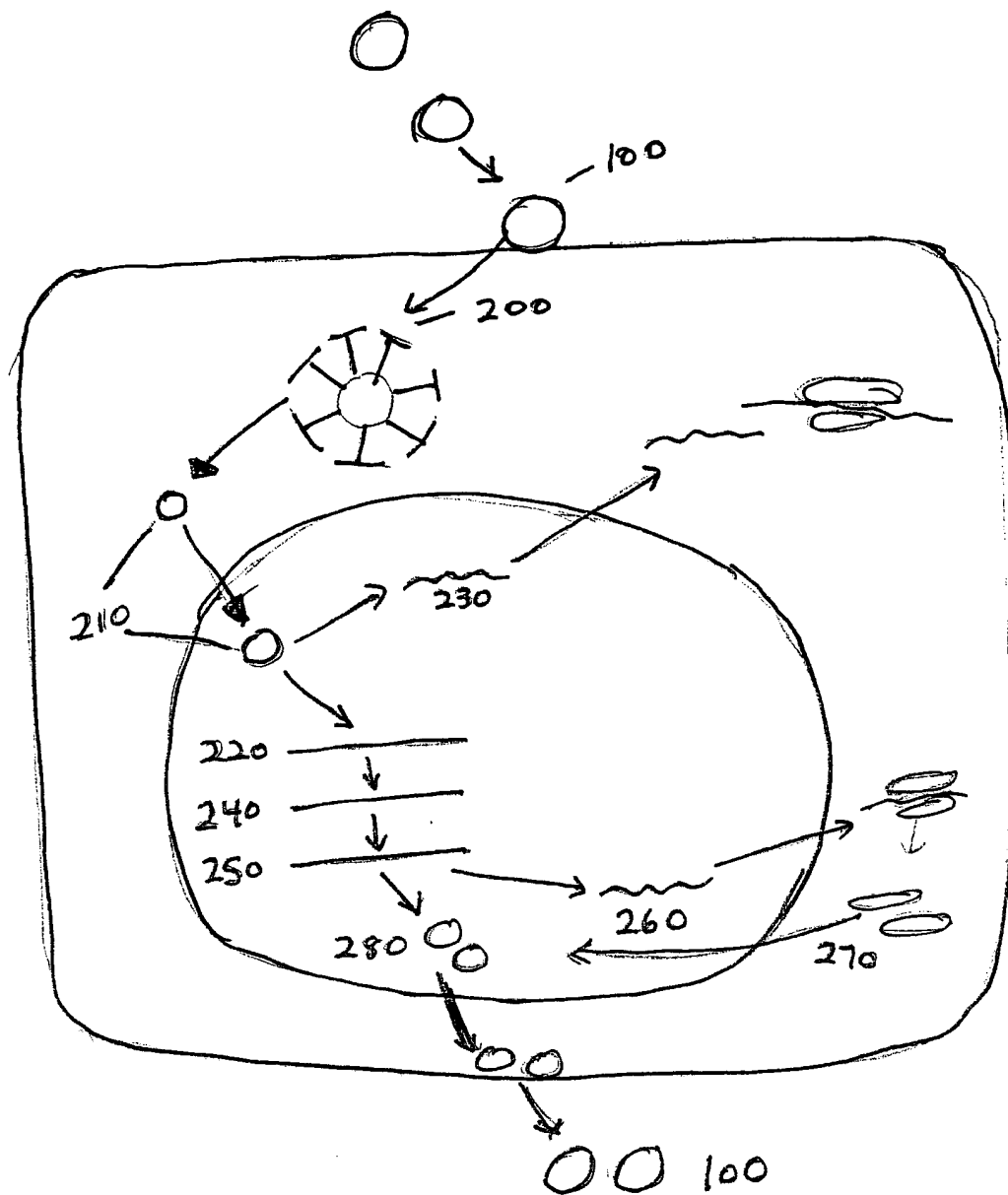


FIGURE 2

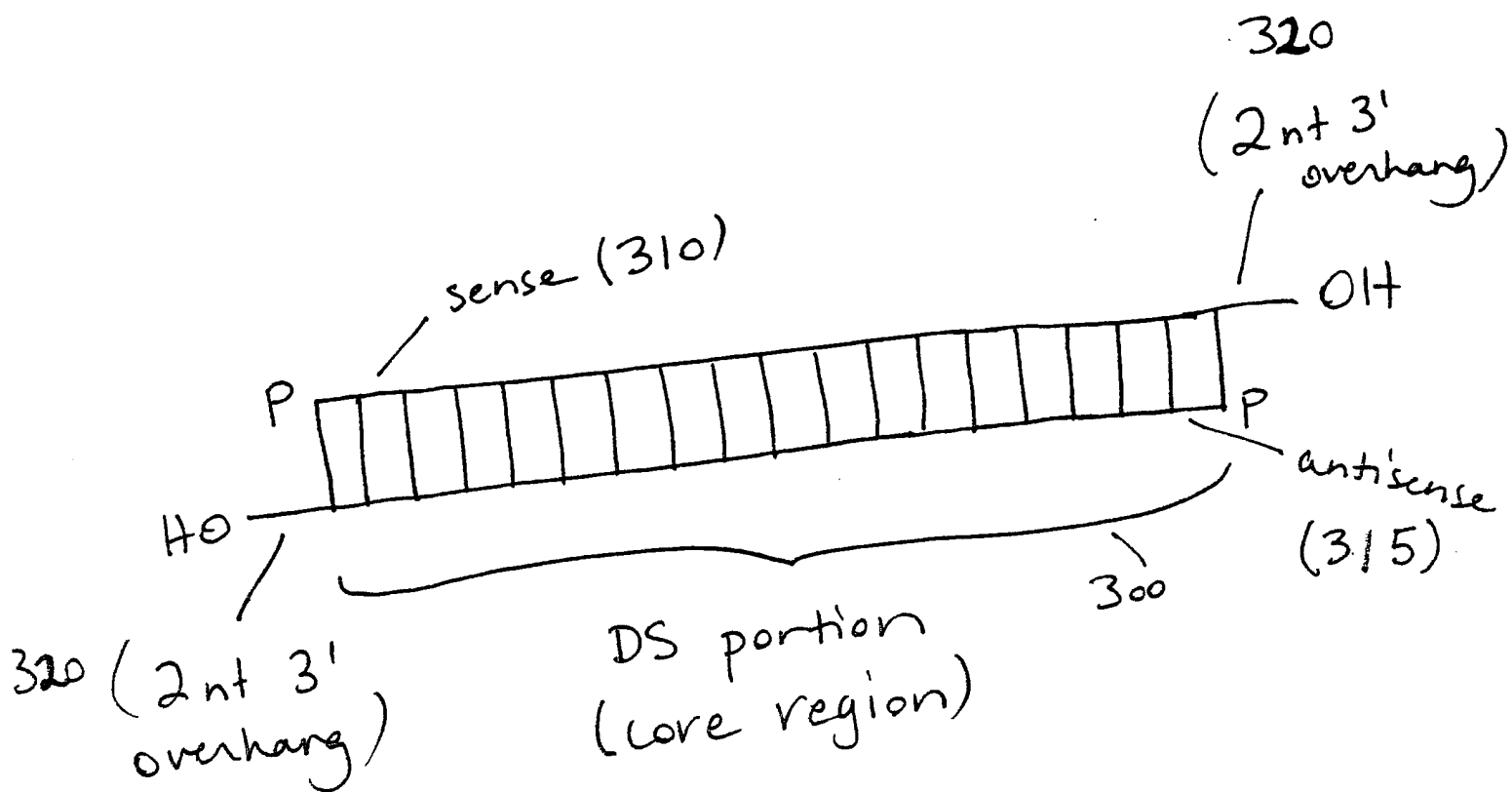


FIGURE 3

RNAi in Drosophila

long dsRNA



siRNA



Helicase?

m7G(5')ppp(5')G-AAAA mRNA

↓ slicing of mRNA by
RISC complex

m7G(5')ppp(5')G-AAAA mRNA



transcript degradation

Figure 4

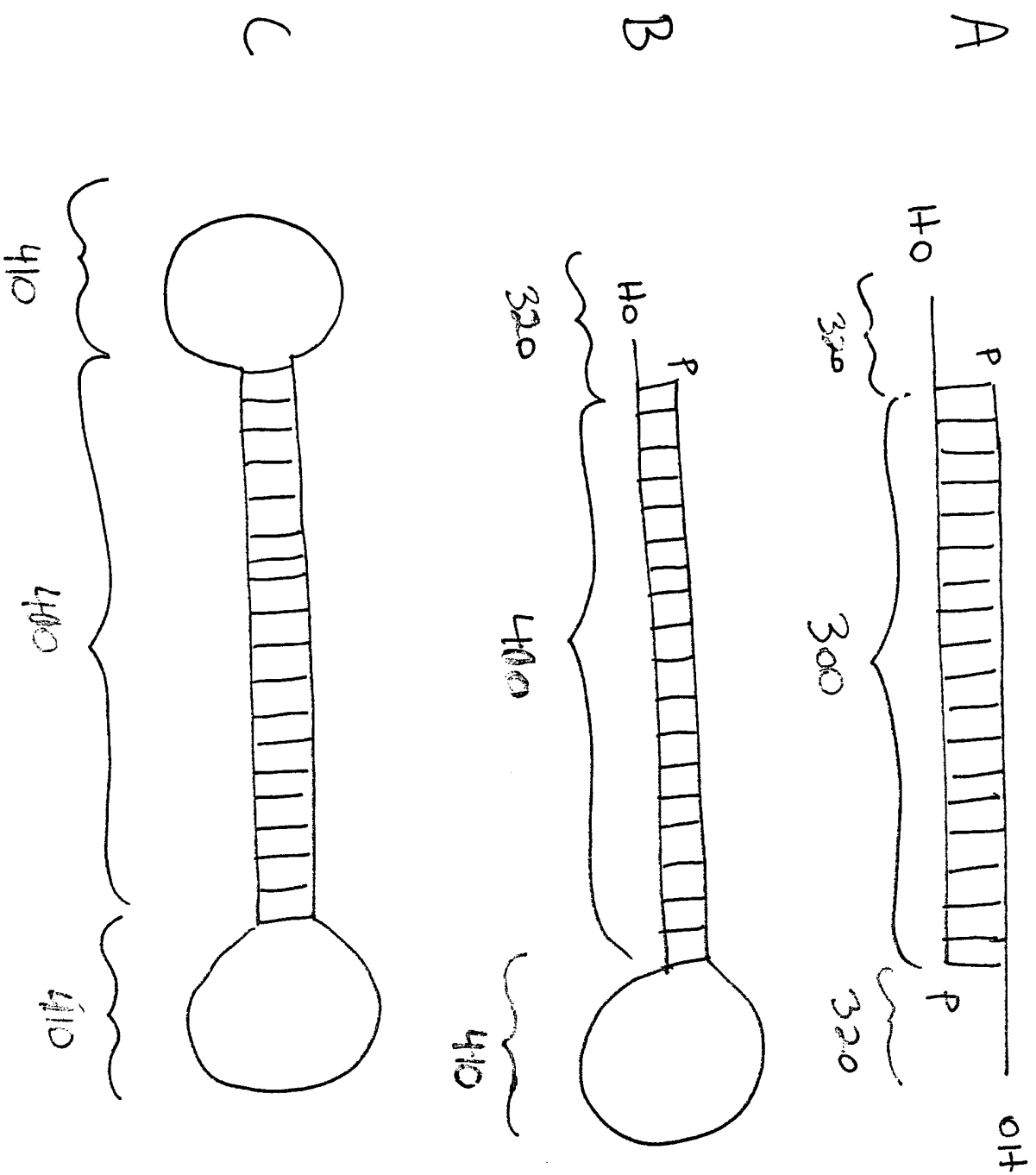


FIGURE 5

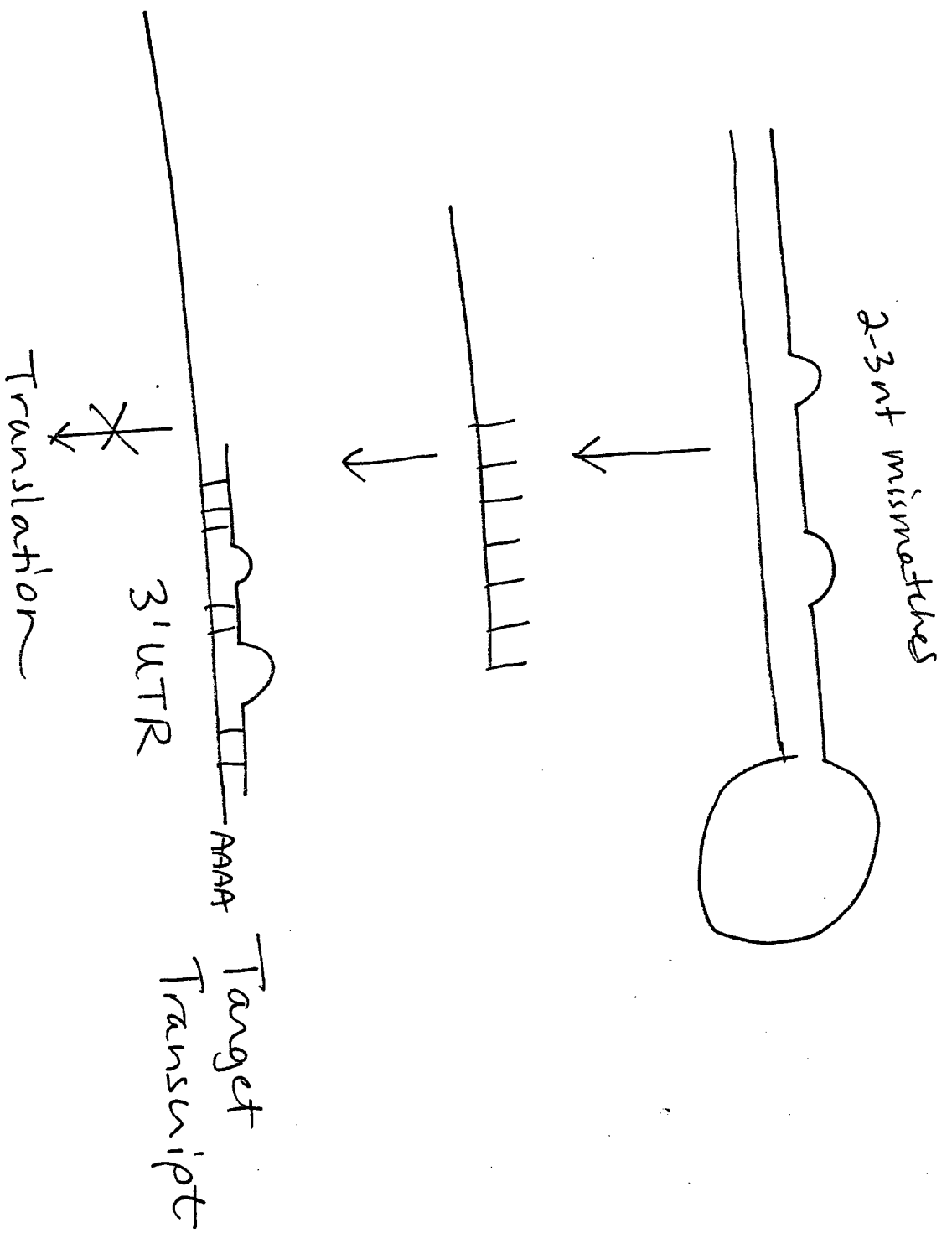


FIGURE 6

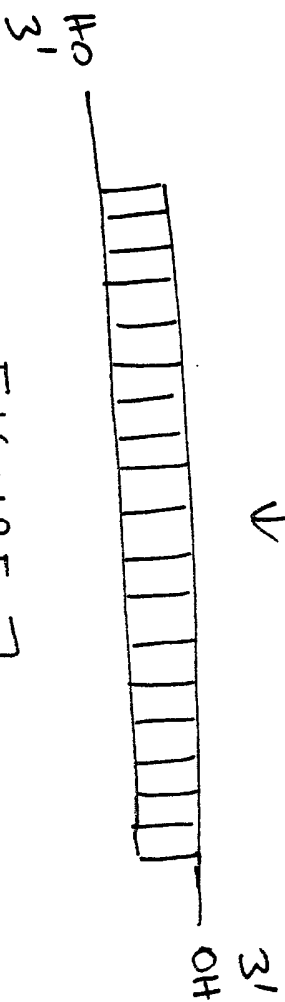
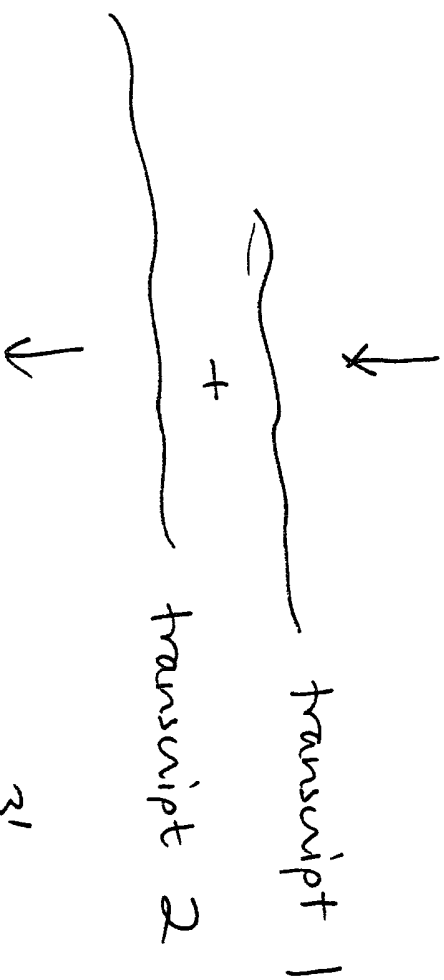
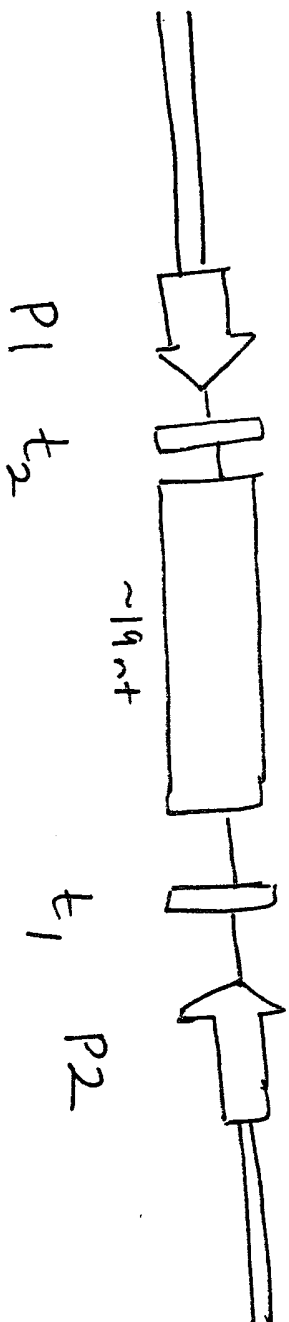


FIGURE 7

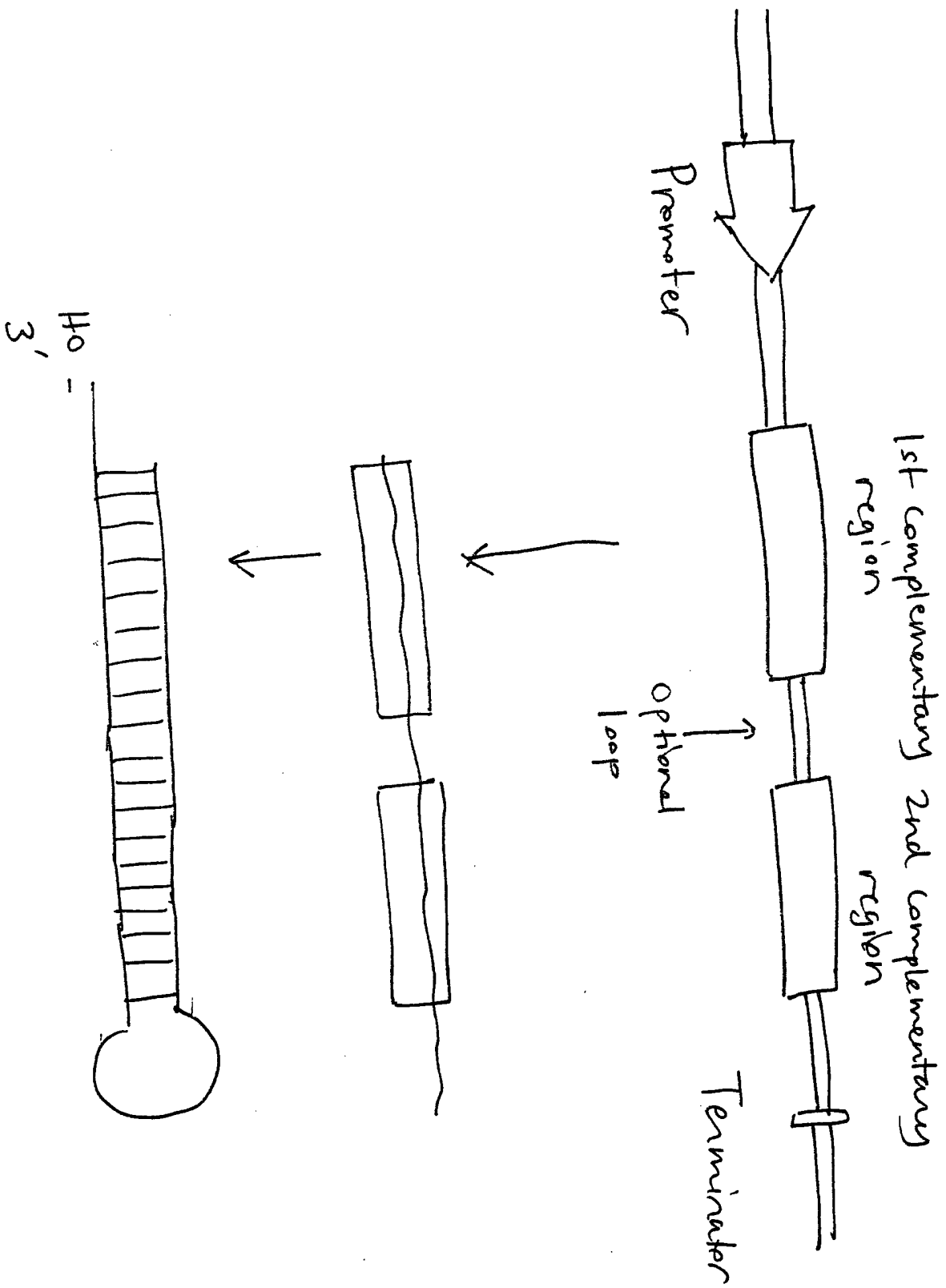


FIGURE 8

Figure 9

CLUSTAL W(1.4) multiple sequence alignment

Shaded area: Highly conserved regions selected as siRNA sequences.

Genbank Acc. No.	Strain			Length
NC_002022	A/Puerto Rico/8/34	H1N1	1934	2233 nt
X17336	A/WSN/33	H1N1	1933	2233 nt
M81579	A/Leningrad/134/17/57	H2N2	1957	2233 nt
AF348174	A/Hong Kong/1/68	H3N2	1968	2209 nt
AF257193	A/Hong Kong/481/97	H5N1	1997	2233 nt
AF257191	A/Hong Kong/1073/99	H9N2	1999	2233 nt

```

NC_002022/- AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
X17336/- AGCGAAAGCAGGTACTGATTCAAAATGGAAGATTTTGTGCGACAATGCTT
M81579/- AGCAAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
AF348174/- -----ATGGAAGATTTTGTGCGACAATGCTT
AF257193/- AGCAAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
AF257191/- AGCAAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT

```

```

NC_002022/- CAATCCCATCATTCGAGCTTGCGGAAAAACAATGAAAGAGTATGGGG
X17336/- CAATCCGATGATTGTGCGAGCTTGCGGAAAAGGCAATGAAAGAGTATGGAG
M81579/- CAATCCGATGATTGTGCGAGCTTGCGGAAAAGGCAATGAAAGAGTATGGAG
AF348174/- CAATCCGATGATTGTGCGAGCTTGCGGAAAAGGCAATGAAAGAGTATGGAG
AF257193/- CAATCCAATGATTGTGCGAGCTTGCGGAAAAGACAATGAAGGAGTATGGGG
AF257191/- CAATCCAATGATTGTGCGAGCTTGCGGAAAAGACAATGAAGGAGTATGGGG

```

```

NC_002022/- AGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACCTCACTTG
X17336/- AGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACCTCACTTG
M81579/- AGGATCGGAAAATCGAAACAAACAAATTTGCAGCAATATGCACCTCACTTG
AF348174/- AGGATCTTAAAATCGAAACAAACAAATTTGCAGCAATATGCACCTCACTTG
AF257193/- AAGATCCGAAATGTTGAAACAAACAAAGTTCGCTGCAATATGCACACACTTA
AF257191/- AAGACCCGAAAATTTGAAACAAATTAAGTTCGCTGCAATATGCACACACTTA

```

```

NC_002022/- GAAGTATGCTTCATGTATTTCAGATTTCCACTTCATCAATGAGCAAGGCCGA
X17336/- GAAGTATGCTTCATGTATTTCAGATTTTCACTTCATCATGAGCAAGGCCGA
M81579/- GAAGTATGCTTCATGTATTTCAGATTTTCACTTCATCAATGAGCAAGGCCGA
AF348174/- GAAGTATGCTTCATGTATTTCAGATTTTCACTTCATCAATGAGCAAGGCCGA
AF257193/- GAAGTATGCTTCATGTATTTCAGACTTCCATTTTCATTGACGAACGAGGCCGA
AF257191/- GAAGTATGCTTCATGTATTTCAGACTTCCATTTTCATTGACGAACGAGGCCGA

```

```

NC_002022/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACCTTTTGAAGCACAGAT
X17336/- GTCAATAATCGTAGAACTTGGGATCCAAATGCACCTTTTGAAGCACAGAT
M81579/- GTCAATAATAGTAGAGCTTGATGATCCAAATGCACCTTTTGAAGCACAGAT
AF348174/- GTCAATAATCGTAGAACTTGGTGATCCAAATGCACCTTTTGAAGCACAGAT
AF257193/- ATCAATAATTGTGGAATCTGGTGATCCGAATGCATTGTTGAAGCACAGGT
AF257191/- ATCAATAATTGTGGAATCTGGTGATCCAAATGCATTGTTGAAGCACAGGT

```

```

NC_002022/- TTGAAATAATCGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAAC
X17336/- TTGAAATAATCGAGGGAAGAGATCGCACAAATAGCCTGGACAGTAGTAAAC
M81579/- TTGAAATAATAGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAAC
AF348174/- TTGAAATAATAGAGGGAAGAGACCGCACAAATGGCCTGGACAGTAGTAAAC
AF257193/- TTGAAATAATTGAAGGAAGAGACCGAGCAATGGCCTGGACAGTGGTGAAT
AF257191/- TTGAAATAATTGAAGGAAGAGACCGAGCAATGGCCTGGACAGTGGTGAAT

```

```

NC_002022/- AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT
X17336/- AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT
M81579/- AGTATTTGCAACACTACAGGAGCTGAGAAACCGAAGTTTCTGCCAGATTT
AF348174/- AGTATTTGCAACACCACAGGAGCTGAGAAACCGAAGTTTCTGCCAGATTT
AF257193/- AGCATCTGCAACACCACAGGAGTCGATAAACCCAAATTTCTCCGGATCT
AF257191/- AGCATCTGCAACACCACAGGAGTCGATAAACCCAAATTTCTCCGGATCT

```

Figure 9

NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	GTATGATTACAAGGAAAATAGATTTCATCGAAATTGGAGTAACAAGGAGAG GTATGATTACAAGAAGAATAGATTTCATCGAAATTGGAGTAACAAGGAGAG GTATGATTACAAGGAGAATAGATTTCATCGAGATTGGAGTGACAAGGAGGG GTATGATTACAAGGAGAATAGATTTCATCGAGATTGGAGTGACAAGGAGAG ATAAGACTACAAGGAAAACCGATTCACTGAAATTGGTGTGACAAGGAGGG ATACGACTACAAGGAAAACCGATTCACTGAAATTGGTGTGACAAGGAGGG
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAAATCTGAGAA
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	ACACACATCCACATTTTCTCGTTCACTGGGGAAGAAATGGCCACAAAGGC ACACACATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACACATCCACATTTTCTCATTCACTGGGGAAGAAATGGCCACAAAGGC ACACACATCCACATTTTCTCATTCACTGGGGAAGAAATGGCCACAAAGGC ACACATATCCACATCTTCTCATTCACTGGAGAAGAAATGGCCACTAAAGC ACACATATCCACATCTTCTCATTCACTGGAGAAGAAATGGCCACTAAAGC
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	CGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAAACCAGGCTAT CGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAAACCAGGCTAT CGACTACACTCTCGATGAGGAAAGCAGGGCTAGGATCAAAACCAGACTAT CGACTACACTCTCGATGAGGAAAGCAGGGCTAGGATCAAAACCAGACTAT TGACTACACCCTTGATGAAGAGAGCAGGGCAAGAATCAAAACCAGACTAT TGACTACACCCTTGATGAAGAGAGCAGGGCAAGAATCAAAACCAGACTAT
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	TCACCATAAGACAAGAAATGGCCAGCAGAGGCCCTCTGGGATTCCCTTCGT TCACCATAAGACAAGAAATGGCTAGCAGAGGCCCTCTGGGATTCCCTTCGT TCACCATAAGACAAGAAATGGCTAGCAGAGGCCCTCTGGGATTCCCTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCCTCTGGGATTCCCTTCGT TCACCATAAGACAAGAAATGGCAAGCAGGGGTCTATGGGATCCCTTCGT TCACCATAAGACAAGAAATGGCAAGCAGGGGTCTATGGGATTCCCTTCGT
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAATCACAGG CAGTCCGAGAGAGGCGAAGAGACAATTGAAGAAAGATTTGAATCACAGG CAGTCCGAAAGAGGCGAAGAAACAATTGAAGAAAGATTTGAATCACAGG CAGTCCGAAAGAGGCGAAGAAACAATTGAAGAAAGATTTGAATCACAGG CAGTCCGAGAGAGGCGAAGAGACAATTGAAGAAAGATTTGAATCACAGG CAGTCCGAGAGAGGCGAAGAGACAATTGAAGAAAGATTTGAATCACAGG
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	AACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC AACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC GACAATGCGCAGGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC GACAATGCGCAGGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC GACCATGCGTAGGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC GACCATGCGTAGGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCC
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT TTGAAAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT TTGAGAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT TTGAGAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT TTGAAAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT TTGAAAATTTTAGAGCCTATGTGGATGGATTGCAACCGAACGGCTACATT
NC_002022/-	GACGCGAAGCTGTCTCAAATGTCCAAAGAAGTAAATGCTAGAATTGAACC

Figure 9

X17336/- M81579/- AF348174/- AF257193/- AF257191/-	GAGGGCAAGCTTTCTCAAATGTCCAAAGAAGTAAATGCTAGAATTGAACC GAGGGCAAGCTTTCTCAAATGTCCAAAGAAGTAAATGCTAAAATTGAACC GAGGGCAAGCTTTCTCAAATGTCCAAAGAAGTGAATGCAAAAATTGAACC GAGGGCAAGCTTTCTCAAATGTCCAAAGAAGTGAACGCCAGAATTGAGCC GAGGGCAAGCTTTCTCAAATGTCCAAAGAAGTGAACGCCAGAATTGAGCC
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	TTTTTTGAAAAACAACACCACGACCCTTAGACTTCCGAATGGGCCTCCCT TTTTTTGAAAAACAACACCACGACCCTTAGACTTCCGGATGGGCCTCCCT TTTTTTGAAAAACAACACCAAGACCAATTAACTTCCGGATGGGCCTCCCT TTTTTTGAAAAACAACACCAAGACCAATTAGACTTCCGGATGGGCCTCCCT ATTTCTGAAGACAACACCACGTCCTCTCAGATTGCCTGATGGACCTCCCT ATTTCTGAAGACAACACCACGTCCTCTCAGATTGCCTGATGGACCTCCCT
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAATTAAGCATT GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAATTAAGCATT GCTCTCAGCGGTCCAAATTCCTGCTGATGGATGCTTTAAATTAAGCATT GTTTTCTCAGCGGTCCAAATTCCTCTGATGGATGCTTTAAATTAAGCATT GCTCCAGCGGTCCAAATTCCTGCTGATGGATGCTCTGAAATTAAGCATT GCTCCAGCGGTCCAAATTCCTGCTGATGGATGCTCTGAAATTAAGCATT
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA GAGGACCCAAGTCAGGAAGGAGAGGGAATACCACTATATGATGCGATCAA GAGGACCCAAGTCAGGAAGGAGAGGGAATACCACTATATGATGCGATCAA GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCGATCAA GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCGATCAA
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC GTGATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	ACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG ACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG ACGAAAAGGGAATAAATCCAAATTATCTGCTGTCATGGAAGCAAGTACTG ACGAAAAGGGAATAAATCCAAATTATCTGCTGTCATGGAAGCAAGTACTG ACGAAAAGGGAATAAATCCAAATTATCTGCTGTCATGGAAGCAAGTACTG ACGAAAAGGGAATAAATCCAAATTATCTGCTGTCATGGAAGCAAGTACTG
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA GCAGAACTGCAGGATATTGAAAATGAGGATAAAAATCCAAAAACAAAGAA GCAGAACTGCAGGATATTGAAAATGAGGATAAAAATCCAAAAACAAAGAA
NC_002022/- X17336/- M81579/- AF348174/- AF257193/- AF257191/-	TATGAAAAAAACAAGTCAGCTAAAAGTGGGCACTTGGTGAGAACATGGCAC TATGAAGAAAAACGAGTCAGCTAAAAGTGGGCACTTGGTGAGAACATGGCAC CATGAAGAAAAACGAGTCAGCTAAAAGTGGGCACTTGGTGAGAACATGGCAC CATGAAGAAAAACGAGTCAGCTAAAAGTGGGCACTTGGTGAGAACATGGCAC CATGAAGAAAAACAAGCAATTAATGTGGGCACTCGGAGAGAATATGGCAC CATGAAGAAAAACAAGCAATTAATGTGGGCACTCGGAGAGAATATGGCAC
NC_002022/- X17336/- M81579/- AF348174/-	CAGAAAAGGTAGACTTTGACGACTGTAAAGATGTAGGTGATTTGAAGCAA CAGAAAAGGTAGACTTTGACGACTGTAAAGATGTAGGTGATTTGAAGCAA CAGAGAAGGTAGACTTTGACGACTGTAGAGATTAAGCGATTTGAAGCAA CAGAGAAGGTAGACTTTGACGACTGTAGAGAGTAAGCGATTTGAAGCAA

Figure 9

AF257193/-	CGGAAAAAGTGGACTTTGAGGACTGCAAAGACATTGATGATCTGAAACAG
AF257191/-	CGGAAAAAGTGGACTTTGAGGACTGCAAAGATATTGGCGATCTGAAACAG
NC_002022/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTCAGAA
X17336/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTCAGAA
M81579/-	TATGATAGTGATGAACCTGAATTAAGGTCACTTTCAAGCTGGATCCAGAA
AF348174/-	TATGATAGTGAGGAACCTGAATTAAGGTCACTTTCAAGCTGGATCCAGAA
AF257193/-	TACCAAGTGATGAGCCAGAGCTTAGATCGCTAGCAAGCTGGATCCAGAA
AF257191/-	TATCAAAGTGATGAGCCAGAGCTCAGATCGCTAGCAAGCTGGATCCAGAG
NC_002022/-	TGAGTTCAACAAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTTG
X17336/-	TGAGTTCAACAAGGCATGCGAACTGACCGATTCAAGCTGGATAGAGCTCG
M81579/-	TGAGTTCAACAAGGCATGCGAGCTGACCGATTCAATCTGGATAGAGCTCG
AF348174/-	TGAGTTCAACAAGGCATGCGAGCTGACCGATTCAATCTGGATAGAGCTCG
AF257193/-	TGAGTTCAACAAGGCATGTGAATTGACCGATTTCGAGCTGGATAGAAGTTG
AF257191/-	TGAGTTCAACAAGGCATGTGAATTGACCGATTTCGAGCTGGATAGAAGTTG
NC_002022/-	ATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGA
X17336/-	ATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGA
M81579/-	ATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGA
AF348174/-	ATGAGATTGGAGAAGAGGTGGCTCCAATTGAATACATTGCAAGCATGAGA
AF257193/-	ATGAGATAGGGGAAGATGTTGCCCAATTGAGCACATTGCAAGCATGAGA
AF257191/-	ATGAGATAGGGGAAGATGTTGCCCAATTGAGCACATTGCAAGCATGAGA
NC_002022/-	AGGAATTATTTACATCAGAGGTGTCTCACTGCAGAGCCACAGAATACAT
X17336/-	AGGAATTATTTACAGCAGAGGTGTCTCATTGCAGAGCCACAGAATACAT
M81579/-	AGGAATTACTTCACAGCAGAGGTGTCTCAGTGCAGAGCCACAGAATATAT
AF348174/-	AGGAATTACTTCACAGCAGAGGTGTCCCATTCGAGAGCCACAGAATATAT
AF257193/-	AGGAACACTTTCACAGCGGAGGTGTCCCATTCGAGGGCTACTGAGTACAT
AF257191/-	AGGAACACTTTCACAGCGGAAGTGTCTCATTGCAGGGCCACTGAGTACAT
NC_002022/-	AATGAAGGGGGTGTACATCAATACTGCCTTACTTAATGCATCTTGTGCAG
X17336/-	AATGAAGGGGGTGTACATCAATACTGCCTTGCTTAATGCATCCTGTGCAG
M81579/-	AATGAAGGGGGTATACATTAATACTGCCTTGCTTAATGCATCCTGTGCAG
AF348174/-	AATGAAGGGGGTATACATTAATACTGCCTTGCTTAATGCATCCTGTGCAG
AF257193/-	AATGAAGGGGGTTTACATAAATACAGCTTTGCTCAATGCATCTTGTGCAG
AF257191/-	AATGAAGGGGGTTTACATAAATACAGCTTTGCTCAATGCATCTTGTGCAG
NC_002022/-	CAATGGATGATTTCCAATTAATTCCAATGATAAGCAAGTGTAGAACTAAG
X17336/-	CAATGGATGATTTCCAATTAATTCCAATGATAAGCAAGTGTAGAACTAAG
M81579/-	CAATGGAAGATTTCCAATTAATTCCAATGATAAGCAATGTAGAACTAAA
AF348174/-	CAATGGACGATTTCCAATTAATTCCAATGATAAGCAAGTGTAGAACTAAA
AF257193/-	CCATGGATGACTTCCAATGATTCCAATGATAAGCAATGCGAGAACAAAA
AF257191/-	CCATGGATGACTTCCAATGATTCCAATGATAAGCAATGCAGAACAAAA
NC_002022/-	GAGGGAAGGCGAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATC
X17336/-	GAGGGAAGGCGAAAGACCAATTTGTAAGGTTTCATCATAAAAGGAAGATC
M81579/-	GAGGGAAGGCGAAAGACCAATTTATATGGTTTCATCATAAAAGGAAGATC
AF348174/-	GAAGGAAGGCGAAAGACCAATTTATATGGTTTCATCATAAAAGGAAGATC
AF257193/-	GAAGGAAGGAGGAAGACAAACCTGTATGGGTTTCAATTATAAAGGAAGGTC
AF257191/-	GAAGGAAGGAAGGACAAACCTGTATGGGTTTCAATTATAAAGGAAGGTC
NC_002022/-	CCACTTAAGGAATGACACCGACGTGGTAACTTTGTGAGCATGGAGTTTTT
X17336/-	CCACTTAAGGAATGACACCGAGTGGTAACTTTGTGAGCATGGAGTTTTT
M81579/-	TCACTTAAGGAATGACACCGACGTGGTAACTTTGTGAGCATGGAGTTTTT
AF348174/-	TCACTTAAGGAATGACACCGACGTGGTAACTTTGTGAGCATGGAGTTTTT
AF257193/-	CCATTTGAGAAATGATACTGACGTGGTGAACCTTTGTGAGTATGGAATTC
AF257191/-	CCATTTGAGAAATGATACTGACGTGGTGAACCTTTGTGAGTATGGAATTC

Figure 9

NC_002022/-	CTCTCACTGACCCAAGACTTGAACCACACAAATGGGAGAAGTACTGTGTT
X17336/-	CCTCACTGACCCAAGACTTGAACCACACAAATGGGAGAAGTACTGTGTT
M81579/-	CTCTCACTGACCCAAGACTTGAGCCACACAAATGGGAGAAGTACTGTGTT
AF348174/-	CTCTCACTGACCCAAGACTTGAGCCACACAAATGGGAGAAGTACTGTGTT
AF257193/-	CGCTTACTGACCCAAGGCTGAGCCACACAAATGGGAGAAGTACTGTGTT
AF257191/-	CGCTTACTGACCCAAGGCTGAGCCACACAAATGGGAGAAGTACTGTGTT
NC_002022/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCCATAGGCCAGGTTTCAAG
X17336/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCCATAGGCCAGGTTTCAAG
M81579/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCCATAGGCCAGGTTTCAAG
AF348174/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCTTATAGGCCAGGTTTCAAG
AF257193/-	CTTGAATATAGGGGAATGCTCTTCCGGACTGCAATAGGTCAGGTGTCAAG
AF257191/-	CTTGAATATAGGGGAATGCTCTTCCGGACTGCAATAGGCCAGGTTTCAAG
NC_002022/-	GCCCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAAAATAAAAATGA
X17336/-	GCCCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAAAATAAAAATGA
M81579/-	GCCCATGTTCTTGTATGTGAGGACAAATGGAACATCAAAGATTAAAAATGA
AF348174/-	GCCCATGTTCTTGTATGTGAGAACAAATGGAACATCAAAGATTAAAAATGA
AF257193/-	GCCCATGTTCTTGTATGTGAGAACCAACGGAACCTCAAAAAATTAAGATGA
AF257191/-	GCCCATGTTCTTGTATGTGAGAACCAACGGAACCTCAAAAAATTAAGATGA
NC_002022/-	AATGGGGAATGGAGATGAGGCGTTGTCTCCTCCAGTCACTTCAACAAATT
X17336/-	AATGGGGATGGAATGAGGCGTTGCCTCCTTCAGTCACTTCAACAAATC
M81579/-	AATGGGGAATGGAGATGAGGCGTTGCCTCCTTCAGTCACTTCAACAAATC
AF348174/-	AATGGGGAATGGAGATGAGGCGTTGCCTCCTTCAGTCACTTCAACAAATC
AF257193/-	AATGGGGATGGAATGAGGCGTGCCTTCTTCAATCTTCAACAGATT
AF257191/-	AATGGGGATGGAATGAGACGCTGCCTTCTTCAATCTTCAACAGATT
NC_002022/-	GAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAGACATGACCAA
X17336/-	GAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAGACATGACCAA
M81579/-	GAGAGTATGATTGAAGCGAGTCCTCTGTCAAAGAGAAAGACATGACCAA
AF348174/-	GAGAGTATGATTGAAGCAGAGTCATCTGTCAAAGAGAAAGACATGACCAA
AF257193/-	GAGAGCATGATCGAGGCTGAGTCTTCTATCAAAGAGAAAGACATGACCAA
AF257191/-	GAGAGCATGATCGAGGCTGAGTCTTCTATCAAAGAGAAAGACATGACCAA
NC_002022/-	AGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTGGGAGAGTCTCCCA
X17336/-	AGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTGGGAGAGTCTCCCA
M81579/-	AGAGTTTTTGGAGAATAAATCAGAAACATGGCCCATTGGGAGAGTCTCCCA
AF348174/-	AGAGTTTTTGGAGAATAAATCAGAAACATGGCCCATTGGGAGAGTCTCCCA
AF257193/-	AGAATTCTTTGAGAACAGATCGGAGACATGGCCATTGGGAGAGTCACTTA
AF257191/-	AGAATTCTTTGAGAACAGATCGGAGACATGGCCATTGGGAGAGTCACTTA
NC_002022/-	AAGGAGTGGAGGAAGGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
X17336/-	AAGGAGTGGAGGAAGGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
M81579/-	AAGGAGTGGAGAAGGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCC
AF348174/-	AAGGAGTGGAGATGGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCC
AF257193/-	AAGGAGTGGAGGAAGGCTCCATCGGGAAGGTCTGCAGGACTTTACTAGCA
AF257191/-	AAGGAGTGGAGGAAGGCTCAATCGGGAAGGTCTGCAGGACTTTACTAGCA
NC_002022/-	AAGTCGGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
X17336/-	AAGTCGGTATTCAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
M81579/-	AAGTCGGTATTCAATAGCCTGTATGCATCTCCACAATAGAAGGATTTTC
AF348174/-	AAGTCGGTATTCAATAGCCTGTATGCATCTCCACAATAGAAGGATTTTC
AF257193/-	AAATCTGTCTTCAACAGCCTATATTCATCTCCACAACCTAGAAGGATTTTC
AF257191/-	AAATCTGTCTTCAACAGCCTATATTCATCTCCACAACCTAGAAGGATTTTC
NC_002022/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
X17336/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC

Figure 9

M81579/-	AGCTGAATCAAGAAAAC	TGCTTCTT	TCGTTCAAGGCTCTTAGGGACAATC
AF348174/-	AGCTGAATCAAGAAAAC	TGCTTCTT	TCGTTCAAGGCTCTTAGGGACAATC
AF257193/-	AGCTGAATCGAGAAAAC	TACTACTCAT	TGTTCAAGCACTTAGGGACAACC
AF257191/-	AGCTGAATCGAGAAAAC	TACTACTCAT	TGTTCAAGCACTTAGGGACAACC
NC_002022/-	TGGAACCTGGGACCTTT	TGATCTTGGGGGGCTATATGAAGCAATTGAGGAG	
X17336/-	TGGAACCTGGGACCTTT	TGATCTTGGGGGGCTATATGAAGCAATTGAGGAG	
M81579/-	TTGAACCTGGGACCTTT	TGATCTTGGGGGGCTATATGAAGCAATTGAGGAG	
AF348174/-	TTGAACCTGGGACCTTT	TGATCTTGGGGGGCTATATGAAGCAATTGAGGAG	
AF257193/-	TGGAACCTGGAACCTTC	GATCTTGAAGGGCTATATGGAGCAATTGAGGAG	
AF257191/-	TGGAACCTGGAACCTTT	TGATCTTGAAGGGCTATATGGAGCAATTGAGGAG	
NC_002022/-	TGCCTAATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
X17336/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
M81579/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
AF348174/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
AF257193/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
AF257191/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTC		
NC_002022/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
X17336/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
M81579/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
AF348174/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
AF257193/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
AF257191/-	CTTCCTTACACATGCATTGAGTAGTTGTGGCAATGCTACTATTTGCTAT		
NC_002022/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 121)	
X17336/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 122)	
M81579/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 123)	
AF348174/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 124)	
AF257193/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 125)	
AF257191/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 126)	

Figure 10

CLUSTAL W(1.4) multiple sequence alignment

Shaded area: selected siRNA sequence.

NC_002022	A/Puerto Rico/8/34	H1N1	1934	2233	nt
X17336	A/WSN/33	H1N1	1933	2233	nt
M21850	A/chicken/FPV/Rostock/34	H7N1	1934	2233	nt
AF156457	A/turkey/California/189/66	H9M2	1966	2140	nt
M26087	A/Equine/London/1416/73	H7N7	1973	2233	nt
M26088	A/gull/Maryland/704/77	H13N6	1977	2233	nt
AF222820	A/swine/Hong Kong/9/98	H9N2	1998	1635	nt

```
NC_002022/- AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
X17336/- AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
M21850/- AGCGAAAGCAGGTACTGATCCAAAATGGAAGATTTTGTGCGACAATGCTT
AF156457/- -----ATGGAAGACTTGTGCGACAATGCTT
M26087/- AGCAAAAGCAGGTACTGATCCAAAATGGAAGACTTTGTGCGACAATGCTT
M26088/- AGCAAAAGCAGGTACTGATCCAAAATGGAAGACTTTGTGCGACAATGCTT
AF222820/- -----
```

```
NC_002022/- CAATCCGATGATTCGAGCTTGCAGGAAAAACAATGAAAGAGTATGGGG
X17336/- CAATCCGATGATTCGAGCTTGCAGGAAAAACAATGAAAGAGTATGGAG
M21850/- CAATCCAATGATCGTCGAGCTTGCAGGAAAAACAATGAAAGAATATGGAG
AF156457/- CAATCCAATGATTCGAGCTTGCAGGAAAAAGCAATGAAAGAATATGGAG
M26087/- CAATCCAATGATCGTCGAGCTTGCAGGAAAAAGCAATGAAAGAATATGGAG
M26088/- CAATCCAATGATCGTCGAGCTTGCAGGAAAAAGCAATGAAAGAATATGGAG
AF222820/- -----
```

```
NC_002022/- AGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTG
X17336/- AGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTG
M21850/- AGGACCGGAAAGATCGAAACAAACAAATTTGCAGCAATATGCACACATTTG
AF156457/- AGGACCGGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTG
M26087/- AGGACCGGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTG
M26088/- AGGACCGGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTG
AF222820/- -----
```

```
NC_002022/- GAAGTATGCTTCATGTATTTCAGATTTCCACTTCATCAATGAGCAAGGCCGA
X17336/- GAAGTGTGCTTCATGTATTTCAGATTTCCACTTCATGATGAGCAAGGCCGA
M21850/- GAAGTGTGCTTCATGTATTTCAGATTTCCACTTCATGATGAGCAAGGCCGA
AF156457/- GAAGTGTGCTTCATGTATTTCAGATTTCCACTTCATGATGAGCAAGGCCGA
M26087/- GAAGTGTGCTTCATGTATTTCAGATTTCCACTTCATGATGAGCAAGGCCGA
M26088/- GAAGTGTGCTTCATGTATTTCAGATTTCCACTTCATGATGAGCAAGGCCGA
AF222820/- -----
```

```
NC_002022/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
X17336/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
M21850/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
AF156457/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
M26087/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
M26088/- GTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGAT
AF222820/- -----
```

```
NC_002022/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
X17336/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
M21850/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
AF156457/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
M26087/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
M26088/- TTGAAATAATCGAGGGAAGAGATCGCACAATGGCCTGGACAGTAGTAAAC
AF222820/- -----
```

Figure 10

NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT AGTATTTGCAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT AGCATTGTGCAAACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT AGCATCTGTAACACTACAGGGGCTGAGAAACCAAAGTTTCTACCAGATTT AGTATCTGCAACACCACAAAGAGCTGAGAAACCAAAGTTTCTACCAGATTT AGCATTGTGCAACACCACAGGAGTTGAGAAGCCAAAGTTTCTACCAGATTT -----
NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTAACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTAACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGAG GTATGATTACAAGGAAAATAGATTCATCGAAATTGGAGTACAAGGAGAG -----
NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAA -----
X17336/- M21850/- NC_002022/- AF156457/- M26087/- M26088/- AF222820/-	ACACACATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACACATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACACATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACATATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACATATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACATATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC ACACATATCCACATTTTCTCATTCACTGGGGAGGAAATGGCCACAAAGGC -----
NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	CGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT CGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT CGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT TGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT GGATTAACCTTGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT GGATTAACCTTGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT AGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACACAGGCTAT -----AGCAAAAGCAGGGCTAGGATCAAACACAGGCTAT
NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT TCACCATAAGACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCTTTTCGT -----
NC_002022/- X17336/- M21850/- AF156457/- M26087/- M26088/- AF222820/-	CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG CAGTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTGAAATCACAGG -----
NC_002022/- X17336/- M21850/- AF156457/-	AACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAAGTTCTCCAGCC AACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAAGTTCTCCAGCC AACATGCGCAGGCTTGCCGACCAAAGTCTCCCGCCGAAGTTCTCCAGCC AACAATGCGCAGGCTTGCCGACCAAAGTCTCCCGCCGAAGTTCTCCAGCC

Figure 10

M26087/-	GACAATGCGCAGGCTTGCCGATTACAGTCTCCCACCGAACTTCTCCAGCC
M26088/-	AACATGCGCAGGCTCGCCGACCAAAGTCTCCCACCGAACTTCTCCAGCC
AF222820/-	AACAATGCGCAGGCTTGCCGACCAAAGTCTCCCACCGAACTTCTCCAGCC
NC_002022/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
X17336/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
M21850/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
AF156457/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
M26087/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
M26088/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
AF222820/-	TTGAAAATTTTAGAGCCTATGTGGATGGATTCTGAACCGAACGGCTACATT
NC_002022/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
X17336/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
M21850/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
AF156457/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
M26087/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
M26088/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
AF222820/-	GAGGGCAAGCTTCTCAAATGTCCAAAGAAGTAAATGCTAGAAATTGAACC
NC_002022/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
X17336/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
M21850/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
AF156457/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
M26087/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
M26088/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
AF222820/-	TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCT
NC_002022/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
X17336/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
M21850/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
AF156457/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
M26087/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
M26088/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
AF222820/-	GTTCTCAGCGGTCCAAATTCCTGCTGATGGATGCCTTAAAATTAAGCATT
NC_002022/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
X17336/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
M21850/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
AF156457/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
M26087/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
M26088/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
AF222820/-	GAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAA
NC_002022/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
X17336/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
M21850/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
AF156457/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
M26087/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
M26088/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
AF222820/-	ATGCATGAGAACATTCTTTGGATGGAAGGAACCCAATGTTGTTAAACCAC
NC_002022/-	ACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
X17336/-	ACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
M21850/-	ATGAGAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
AF156457/-	ATGAGAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
M26087/-	ATGAGAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
M26088/-	ATGAGAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG
AF222820/-	ATGAGAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAAGCAAGTACTG

Figure 10

NC_002022/-	GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA
X17336/-	GCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA
M21850/-	GCAGAACTGCAGGATATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA
AF156457/-	GCAGAACTGCAGGATATTGAGAATGAGGAGAAAATTCCAAAGACTAAAAA
M26087/-	GCAGAACTGCAGGACCTTGAAAAGGAGAAAATCCCAAGACCAAGAA
M26088/-	GCAGAACTGCAGGATATTGAAAATGAGGAGCAAGATTCCAAAGACTAAAAA
AF222820/-	GCAGAACTGCAGGACATTGAAAATGAGGAGCAAGATTCCAAAGACTAAAAA
NC_002022/-	TATGAAAAAAACAAGTCAGCTAAAGTGGGCACCTGGTGAGAACATGGCAC
X17336/-	TATGAAAGAAAACAGTCAGTTAAAGTGGGCACCTGGTGAGAACATGGCAC
M21850/-	TATGAAAGAAAACAAGCCAGTTAAAGTGGGCACCTGGTGAGAACATGGCAC
AF156457/-	TATGAAAGAAAACAAGCCAAATTAAAGTGGGCACCTGGTGAGAACATGGCAC
M26087/-	TATGAAAAAAACAAGTCAATTCAATGGGCACCTGGTGAGAACATGGCAC
M26088/-	CATGAAGAAAACAAGCCAAATTAAAGTGGGCACCTGGTGAGAACATGGCAC
AF222820/-	CATGAAGAAAACAAGCCAAATTAAAGTGGGCATTAGGTGAGAACATGGCAC
NC_002022/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTTCAGAA
X17336/-	CAGAAAAGGTAGACTTTGAGGATTGTAAAGATGTAGGCGATTGGAAGCAA
M21850/-	CAGAGAAAAGTAGACTTTGAGGATTGCAAGGACATTAGCGATCTGAAGCAA
NC_002022/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTTCAGAA
AF156457/-	CAGAAAAGGTGGATTTTGAGGACTGCAAGGATGTCAGCGATCTGAAGCAA
M26087/-	CAGAGAAAAGTGGATTTTGAGGATTGTAAAGACATCAGTGATTTCGAACAG
M26088/-	CAGAGAAAAGTGGACTTTGAAGATTGCAAGGATGTCAGCGATTTCGAACAG
AF222820/-	CAGAGAAAAGTGGACTTTGAGGATTGCAAGACGTTAGTGACCTGAACCAA
NC_002022/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTTCAGAA
X17336/-	TATGATAGTGATGAACCAGAATTGAGGTCGCTTGCAAGTTGGATTTCAGAA
M21850/-	TATGACAGTGATGACCCAGAACAGAGATCACTAGCCAGTTGGATTTCAGAG
AF156457/-	TATGACAGTGATGAACCGAACCAGAGATCGCTTGCAAGTTGGATTTCAGAG
M26087/-	TATGACAGTGATGAGCCAGAAACAAGGTCCTTGCAAGTTGGATTTCAGAG
M26088/-	TATGACAGTGATGAGCCAGAACAAAGGTCGCTAGCAAGTTGGATTTCAGAG
AF222820/-	TATGATAGTGATGAACCAGAGCCCAAATCGCTAGCAAGTTGGATTTCAGAG
NC_002022/-	TGAGTTCAACAAGGCATGCGAACTGACAGATTCAAGCTGGATAGAGCTTG
X17336/-	TGAGTTCAACAAGGCATGTGAAGTACCGATTCAAGCTGGATAGAGCTTG
M21850/-	TGAATTCAACAAGGCATGTGAGCTGACCGATTTCAGGTTGGATAGAACTTG
AF156457/-	TGAGTTCAACAAGGCATGTGAAGTACCTGATTCAAGCTGGATAGAGCTTG
M26087/-	TGAGTTCAACAAGCTTGTGAGCTGACAGATTCAAGCTGGATAGAGCTTG
M26088/-	TGAATTCAACAAGCTTGTGAATTGACTGATTCAAGCTGGATAGAACTCG
AF222820/-	TGAATTCAACAAGGCATGTGAGTTGACCGATTCAAGCTGGATTAGAACTTG
NC_002022/-	ATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGA
X17336/-	ATGAGATTGGAGAAGATGCGGCTCCAATTGAACACATTGCAAGCATGAGA
M21850/-	ATGAATATGGAGAAGATGTAGCCCAATTGAGCACATTGCAAGCATGAGG
AF156457/-	AGGAGATTGGGGAAGATGTGCCCCAATTGAGCACATTGCAAGCATGAGG
M26087/-	ATGAATATTGGGAGGATGTGCCCCAATTGAACACATTGCGAGCATGAGG
M26088/-	ATGAATATGGGGAAATGTGCCCCAATGAGCAATTGCAAGCATGAGG
AF222820/-	ATGAATATGGAGAAGATGTGCTCCAATGAGCACATTGCGAGCATGAGA
NC_002022/-	AGGAATTATTTACATCAGAGGTGTCTCACTGCAGAGCCACAGAATACAT
X17336/-	AGGAATTATTTACAGCAGAGGTGTCTCACTGCAGAGCCACAGAATACAT
M21850/-	AGAAAATATTTACAGCGGAAGTGTCTCACTGCAGAGCCACAGATACAT
AF156457/-	AGGAATTATTTACAGCGGAGGTGTCTCACTGTAGAGCCACAGAATACAT
M26087/-	AGGAATTATTTTACTGCTGAGGTTCCTCATGTAGAGCAACTGAATAAT
M26088/-	AGGAATTATTTTACAGCTGAAGTGTCTCACTGCAGGGCAACAGAGTACAT
AF222820/-	AGGAATTATTTTACAGCAGAGGTGTCTCACTGCAGGGCTACTGAGTAAT
NC_002022/-	AATGAAGGGGGTGTACATCAATACTGCCTTACTTAATGCATCTTGTGCAG
X17336/-	AATGAAGGGGGTGTACATCAATACTGCCTTCTTAATGCATCTTGTGCAG

Figure 10

M21850/-	AATGAAAGGGGTATACATTAACACGGCCTTGCTCAATGCATCTTGTGCAG
AF156457/-	AATGAAAGGGGTATACATCAACTGCTTGCTCAATGCATCCTGTGCGG
M26087/-	AATGAAGGGAGTATACATCAACACTGCTTGCTCAATGCATCCTTGCTG
M26088/-	AATGAAGGGAGTGTACATTAACCTCAGCTTTACTCAAAGCTCTTGTGCAG
AF222820/-	AATGAAGGGAGTGTATTAACACAGCCTTGCTCAATGCATCTTGTGCAG
NC_002022/-	CAATGGATGATTTCCAATTAATTCCAATGATAAGCAAGTGTAGAACTAAG
X17336/-	CAATGGATGATTTCCAATTAATTCCAATGATAAGCAAGTGTAGAACTAAG
M21850/-	CTATGGATGACTTCCAGCTGATCCAATGATAAGCAAATGAGGACCAA
AF156457/-	CTATGGATGACTTCAACTCATTCCAATGATCAGCAAGTGTAGAACTAAA
M26087/-	CCATGGATGACTTCCAATTAATCCCATGATAAGCAAATGAGGACCAAG
M26088/-	CCATGGATGATTTTCAGTTGATCCAATGATAAGCAAATGCAGAACCAA
AF222820/-	CCATGGATGACTTCCAATTGATTCCAATGATAAGCAAATGCAGAACAAA
NC_002022/-	GAGGGAAGGCGAAAGACCAACTTGTATGGTTTCATCATAAAAGGAAGATC
X17336/-	GAGGGAAGGCGAAAGACCAATTTGTAAGGTTTCATCATAAAAGGAAGATC
M21850/-	GAGGGAAGACCGAAGACCAATCTGTATGGATTTCATTATAAAAGGAAGATC
AF156457/-	GAGGGAAGAAAGAAAGACAAATTTGTATGGTTTCATTATAAAAGGAGATC
M26087/-	GAGGGAAGAAAGAAAGACAAATTTGTATGGATTTCATCATAAAAGGAAGCTC
M26088/-	GAGGGAAGACCGAAACAAATTTGTATGGATTTCATCATAAAAGGAAGGTC
AF222820/-	GAGGGAAGACCGAAACAACTGTATGGTTTCATTATCAAGGGAAGGTC
NC_002022/-	CCACTTAAGGAATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTT
X17336/-	CCACTTAAGGAATGACACCGATGTGGTAAACTTTGTGAGCATGGAGTTTT
M21850/-	CCACTTGAGGAATGATCTGATCTGGTCAATTTTGTGAGCATGGAGTTCT
AF156457/-	CCACTTGAGGAAGGACACCGATGTGGTAAACTTTGTGAGCATGGAGTTTT
M26087/-	CCATTTAAGGAATGACACTGACGTGGTAAACTTTGTGAGCATGGAGTTTT
M26088/-	CCATTTGAGGAATGATCTGATGTGGTCAATTTTGTGAGCATGGAATTTT
AF222820/-	CCATTTGAGGAATGATCTGATGTGGTAAACTTTGTGAGCATGGAATTTT
NC_002022/-	CTCTCACTGACCCAAGACTTGAACCACACAAATGGGAGAAGTACTGTGTT
X17336/-	CTCTCACTGACCCAAGACTTGAACCACACAAATGGGAGAAGTACTGTGTT
M21850/-	CTCTCACTGACCCGAGGCTTGAACCCACACAAATGGGAGAAGTACTGTGTT
AF156457/-	CTCTCACTGACCCGAGGCTTGAACCCACAAATGGGAGAAGTACTGTGTT
M26087/-	CTCTCACCGATCCAAGACTTGAACCCACACAAATGGGAGAAGTACTGTGTT
M26088/-	CTCTTACTGACCCTAGAATTAAGAACACACAAATGGGAGAAGTACTGTGTT
AF222820/-	CTCTTACAGACCCGAAACTGGAACCACACAAATGGGAGAAGTACTGTGTT
NC_002022/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCCATAGGCCAGGTTTCAAG
X17336/-	CTTGAGATAGGAGATATGCTTCTAAGAAGTGCCATAGGCCAGTGTCAAG
M21850/-	CTTGAAATAGGAGACATGCTCTCTGGAGTGCATAGGCCAAGTATCAAG
AF156457/-	CTTGAAATAGGGGACATGCTTCTAAGAAGTGCCATAGGCCAAGTTTCAAG
M26087/-	CTTGAAATAGGAGACATGCTCTCTAAGAAGTGCTGTAGGCCAAGTGTCAAG
M26088/-	CTTGAAATAGGGGATATGCTCTCTAGAACGCAATAGGCCAAGTTTCAAG
AF222820/-	CTTGAAATAGGGGACATGCTCTCTGAGAACTCAATAGGCCAGGTTTCAAG
NC_002022/-	GCCCCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAAATTAAAATGA
X17336/-	GCCCCATGTTCTTGTATGTGAGGACAAATGGAACCTCAAAAATTAAAATGA
M21850/-	GCCCCATGTTCTTGTATGTGAGAACCAATGGAACCTCAAAAATCAAGATGA
AF156457/-	GCCCCATGTTCTTGTATGTGAGAACCAATGGGACCTCAAAAATCAAAATGA
M26087/-	ACCCATGTTTCTTGTATGTGAGAACCAATGGGACCTCAAAAATTAAAATGA
M26088/-	ACCCATGTTTCTTGTATGTGACAAACCAATGGAACCTCAAAATGAAATGA
AF222820/-	GCCCCATGTTCTTCTAGGTGAGAACCAATGGAACCTCAAAAATTAAAATGA
NC_002022/-	AATGGGGAATGGAGATGAGGCGTTGTCTCTCCAGTCACTTCAACAAATT
X17336/-	AATGGGGAATGGAGATGAGGCGTTGTCTCTCCAGTCACTTCAACAAATT
M21850/-	AATGGGGATGGAGATGAGACGTTGCTCTCTCCAGTCCCTTCAACAGGTT
AF156457/-	AATGGGGATGGAAATGAGACGCTGTCTCTCCAGTCCCTTCAACAAATT
M26087/-	AATGGGGAATGGAAATGAGGCGTTGCTCTCTCCAGTCTTACAGCAATT
M26088/-	AATGGGGATGGAGATGAGGCGTTGTCTCTCTCAATCCCTCCAGCAAAAT

Figure 10

AF222820/-	AATGGGGAATGGAGATGAGGCGTTGCTCCTTCAATCTCTTCAACAAATT
NC_002022/-	GAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAGACATGACCAA
X17336/-	GAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGGAGAAAGACATGACCAA
M21850/-	GAAAGCATGCTTGAAGCTGAGTCCTCTGTCAAAGGAGAAAGACATGACTAA
AF156457/-	GAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGGAGAAAGACATGACCAA
M26087/-	GAAAGCATGCTTGAAGCTGAGTCCTCTGTCAAAGGAAAGACATGACCAA
M26088/-	GAAAGCATGATTGAGGCGAGTCCTCTGTCAAAGGAAAGACATGACTAA
AF222820/-	GAGAGCATGATTGAAGCAGAGTCCTCTTCAAAGAGAAAGACATGACCAA
NC_002022/-	AGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCTCCCA
X17336/-	AGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCTCCCA
M21850/-	GAAATCTTTGAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCTCCCA
AF156457/-	AGAGTTCTTTGAGAACAAATCAGAAACATGGCCCATTTGGAGAGTCTCCCA
M26087/-	AGAATCTTTGAGAACAAATCGGAGACATGGCCCATTTGGAGAGTCTCCCA
M26088/-	AGAATCTTTGAGAACAAATCGGAGACATGGCCCATTTGGAGAGTCTCCCA
AF222820/-	AGAATCTTTGAGAACAAATCGGAGACATGGCCCATTTGGAGAGTCTCCCA
NC_002022/-	AAGGAGTGGAGGAAAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
X17336/-	AAGGAGTGGAGGAAAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
M21850/-	AAGGAGTGGAAAGGAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
AF156457/-	AAGGAGTGGAGGAAAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
M26087/-	AAGGAGTGGAAAGGAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
M26088/-	AAGGAGTGGAAAGGAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
AF222820/-	AAGGAGTGGAGGAAAGTTCCATTGGGAAGGTCTGCAGGACTTTATTAGCA
NC_002022/-	AAGTCGGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
X17336/-	AAGTCGGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
M21850/-	AAGTCTGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
AF156457/-	AAGTCTGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
M26087/-	AAATCTGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
M26088/-	AAGTCTGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
AF222820/-	AAGTCTGTATTTAACAGCTTGTATGCATCTCCACAACCTAGAAGGATTTTC
NC_002022/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
X17336/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
M21850/-	AGCGGAATCTAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
AF156457/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
M26087/-	AGCTGAATCTAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
M26088/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
AF222820/-	AGCTGAATCAAGAAAACCTGCTTCTTATCGTTTCAGGCTCTTAGGGACAATC
NC_002022/-	TGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAG
X17336/-	TGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAG
M21850/-	TGGAACCTGGGAACCTTTGATCTTGGAGGGCTATATGGAGCAATTGAGGAG
AF156457/-	TGGAACCTGGGAACCTTTGATCTTGGAGGGCTATATGGAGCAATTGAGGAG
M26087/-	TGGAACCTGGGAACCTTTGATCTTGGAGGGCTATATGAATCAATTGAGGAG
M26088/-	TGGAACCTGGGACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAG
AF222820/-	TGGAACCTGGGAACCTTTGATCTTGGGGGGCTATATGAAGCAATTGAGGAG
NC_002022/-	TGCCTAATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
X17336/-	TGCCTAATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
M21850/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
AF156457/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
M26087/-	TGTCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
M26088/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
AF222820/-	TGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCATCTTGGTTCAACTC
NC_002022/-	CTTCCTTACACATGCATTGAGTTAGTTGTGGCAGTGCTACTATTGCTAT

Figure 10

X17336/-	CTTCCTCACACATGCATTGAGATAGTTGTGGCAATGCTACTATTTGCTAT	
M21850/-	CTTCCTCACACATGCAGTGAATAGTTGTGGCAATGCTACTATTTGCTAT	
AF156457/-	CTTCCTCACACATG-----	
M26087/-	CTTCCTTACACATGCACTAAAGTAGTTGTGGCAATGCTACTATTTGCTAT	
M26088/-	CTTCCTCACACATGCAGTGAATAGTTGTGGCAATGCTACTATTTGCTAT	
AF222820/-	C-----	
NC_002022/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 127)
X17336/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 128)
M21850/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 129)
AF156457/-	-----	(SEQ ID NO: 130)
M26087/-	CCATACTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 131)
M26088/-	ACATCTGTCCAAAAAAGTACCTTGTTTCTACT--	(SEQ ID NO: 132)
AF222820/-	-----	(SEQ ID NO: 133)

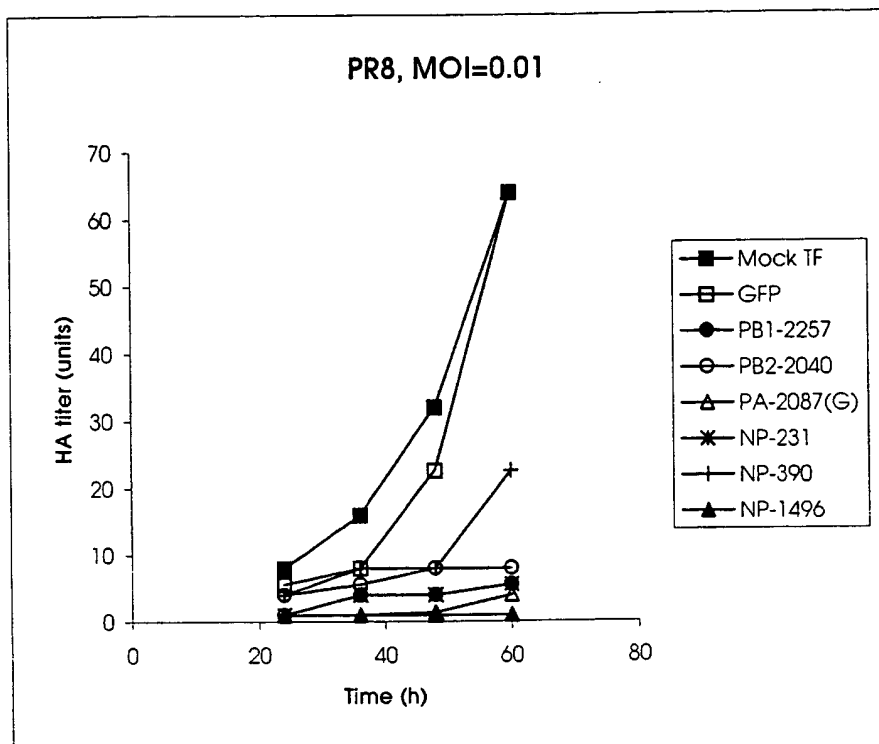


FIGURE 11A

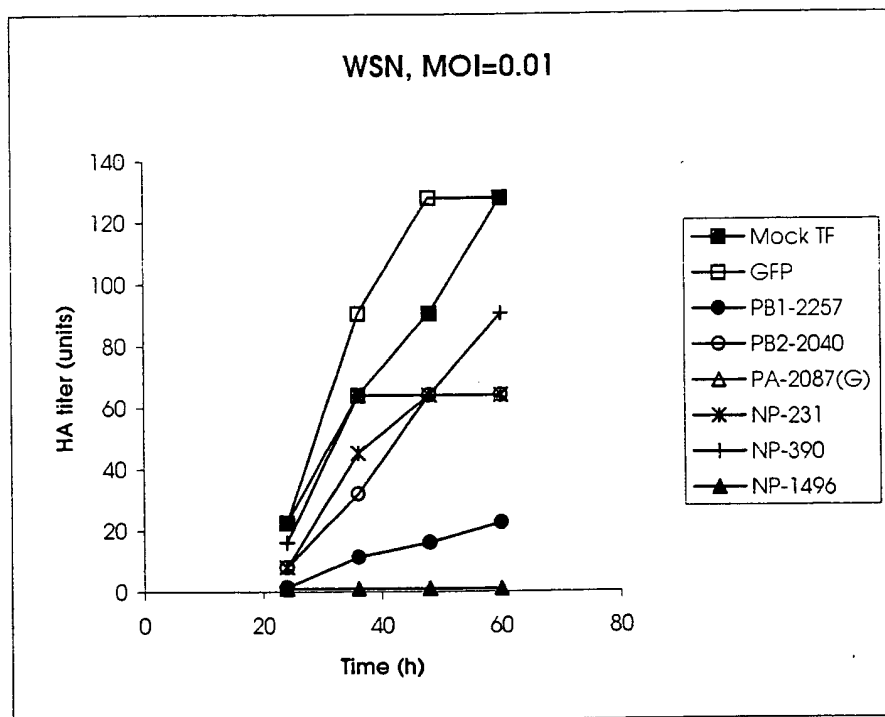
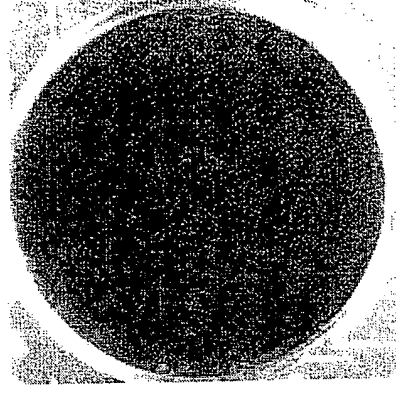
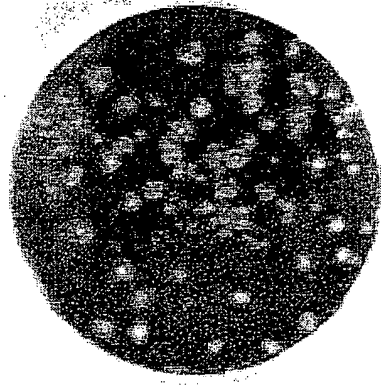


FIGURE 11B

Potent inhibition of influenza A viral replication by NP-1496 siRNA



Mock transfection		NP-1496 siRNA	Fold difference
		2.5 nmole	
MOI=0.001	6x10 ⁵ PFU/ml	<20 PFU/ml	3x10 ⁴
MOI=0.1	1x10 ⁶ PFU/ml	5x10 ³ PFU/ml	2x10 ³

FIGURE 11C

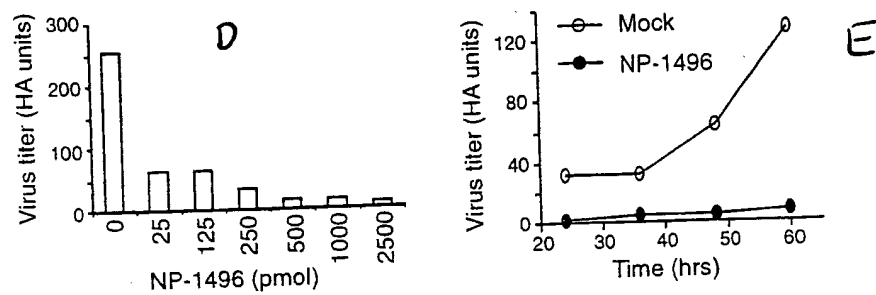


Figure 11

Figure 12

PR8 (H1N1)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGT	
WSN (H1N1)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Lenn. (H2N2)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
HK (H3N2)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Memphis (H3N2)	TCTCAGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
HK (H5N1)	TCTCAGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Duck (H10N7)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Equine (H7N7)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGC	
Whale (H13N2)	TCTCAGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Chicken (H9N2)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
Swine (H4N6)	TCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCCTCCTTTGACATGAGT	
PR8 (H1N1)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 134)		
WSN (H1N1)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 135)		
Lenn. (H2N2)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 136)		
HK (H3N2)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 137)		
Memphis (H3N2)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 138)		
HK (H5N1)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 139)		
Duck (H10N7)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 140)		
Equine (H7N7)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 141)		
Whale (H13N2)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 142)		
Chicken (H9N2)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 143)		
Swine (H4N6)	AATGAAGGATCTTTATTTCTTCGGAGACAATGCAGAGGAGTACGACAATTA	(SEQ ID
NO: 144)		

Summary of the inhibition effect of siRNAs on influenza A virus production

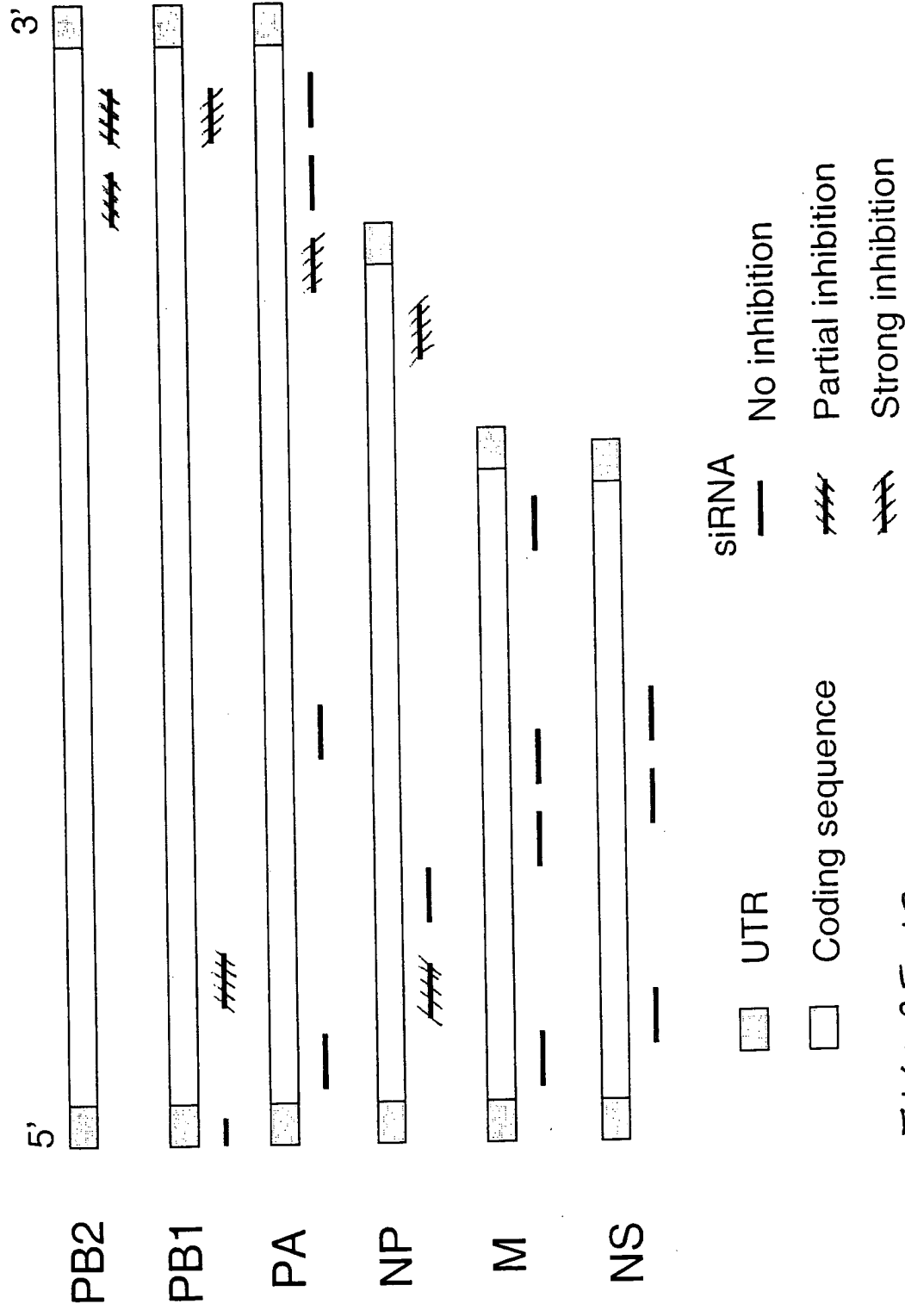
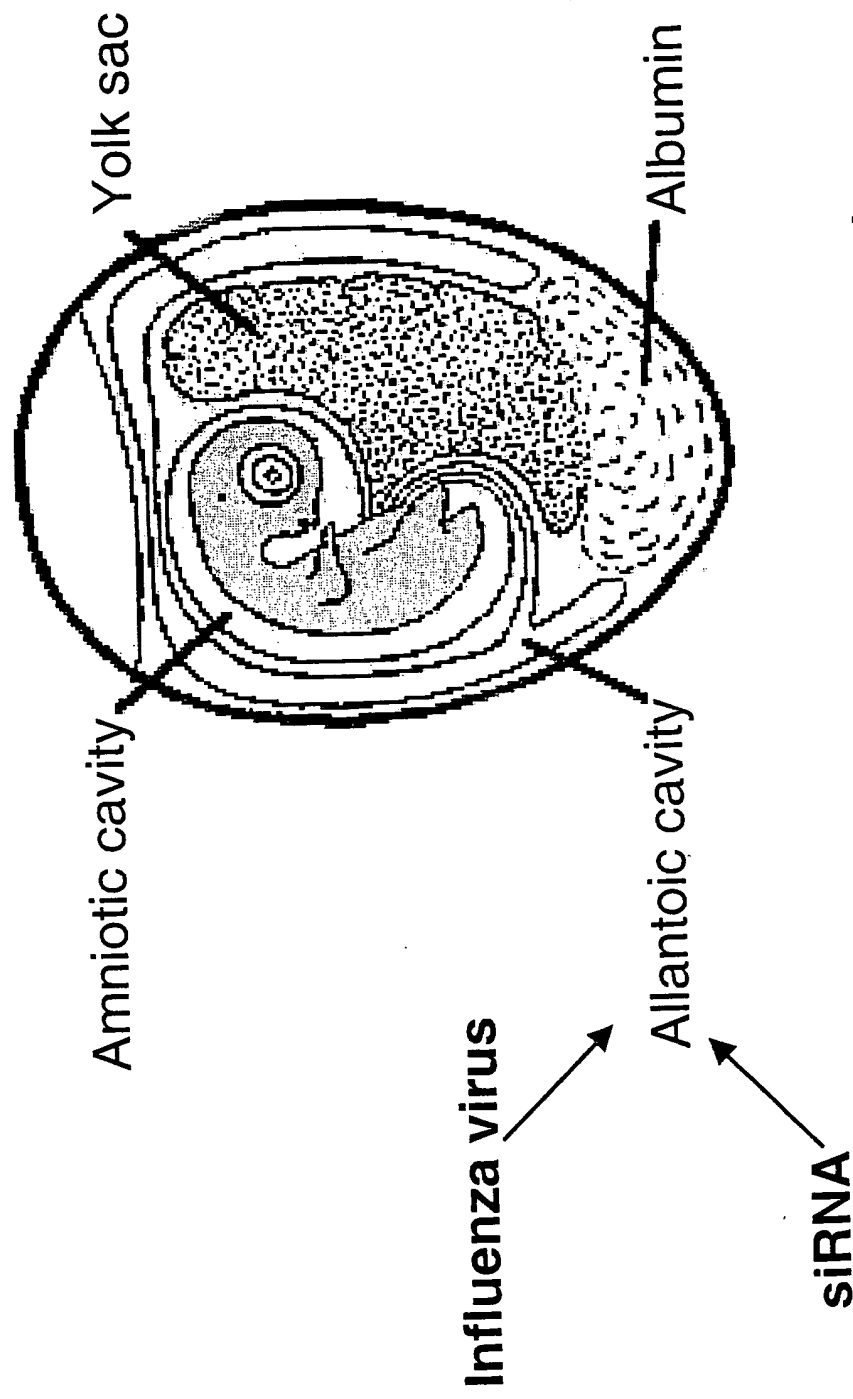


FIGURE 13



10-day old fertilized chicken egg

FIGURE 14 A

The inhibition of influenza A virus replication in chicken embryos

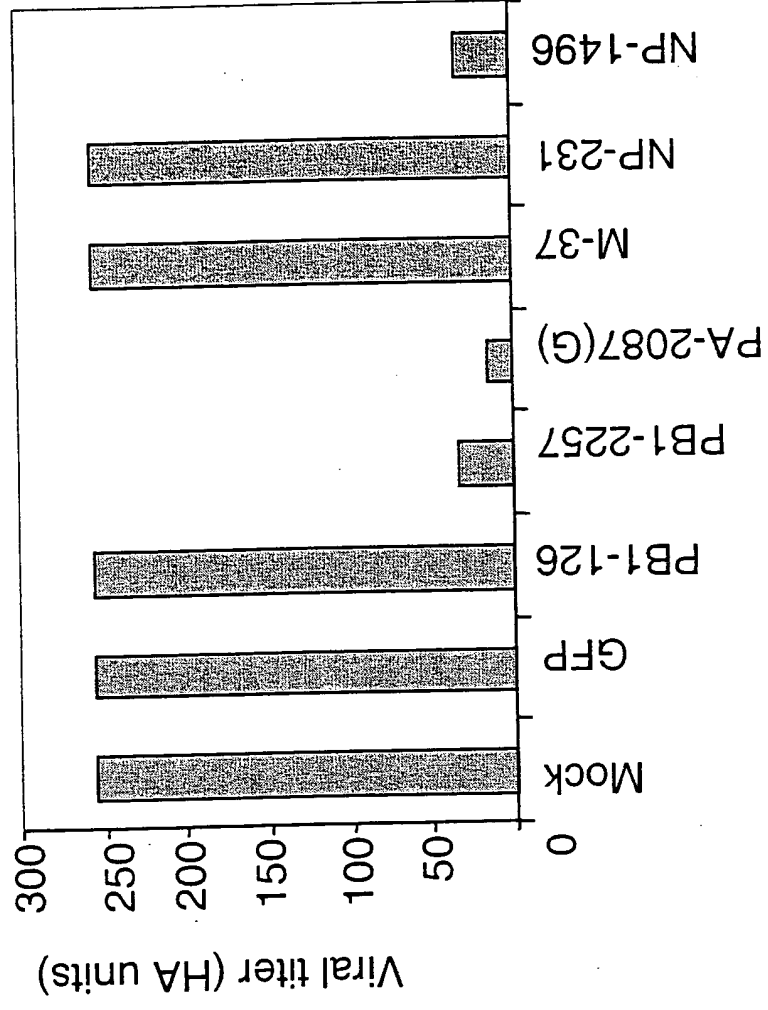


FIGURE 14B

Nucleocapsid protein

RNA-binding protein pivotal to virus replication

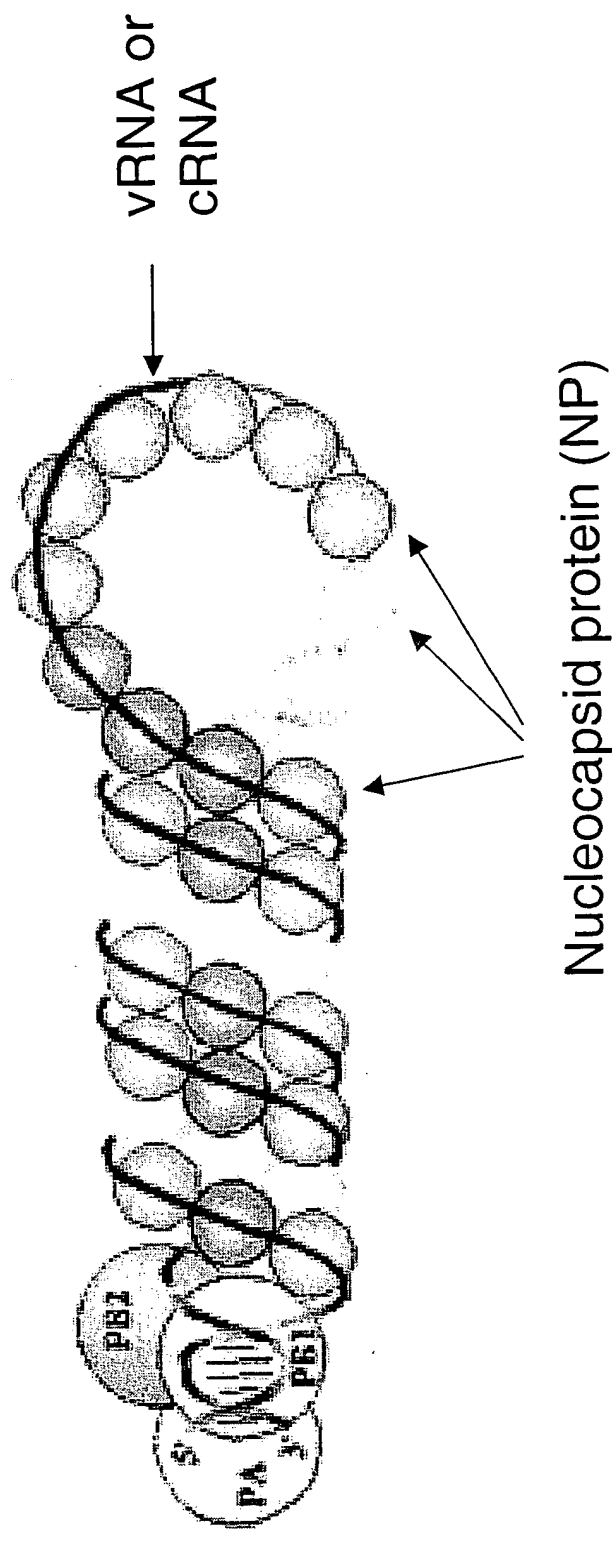


FIGURE 15

Figure 16A

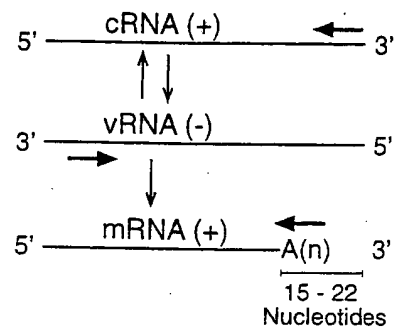


Diagram of influenza virus virion RNA (vRNA), mRNA and full-length cRNA or template RNA

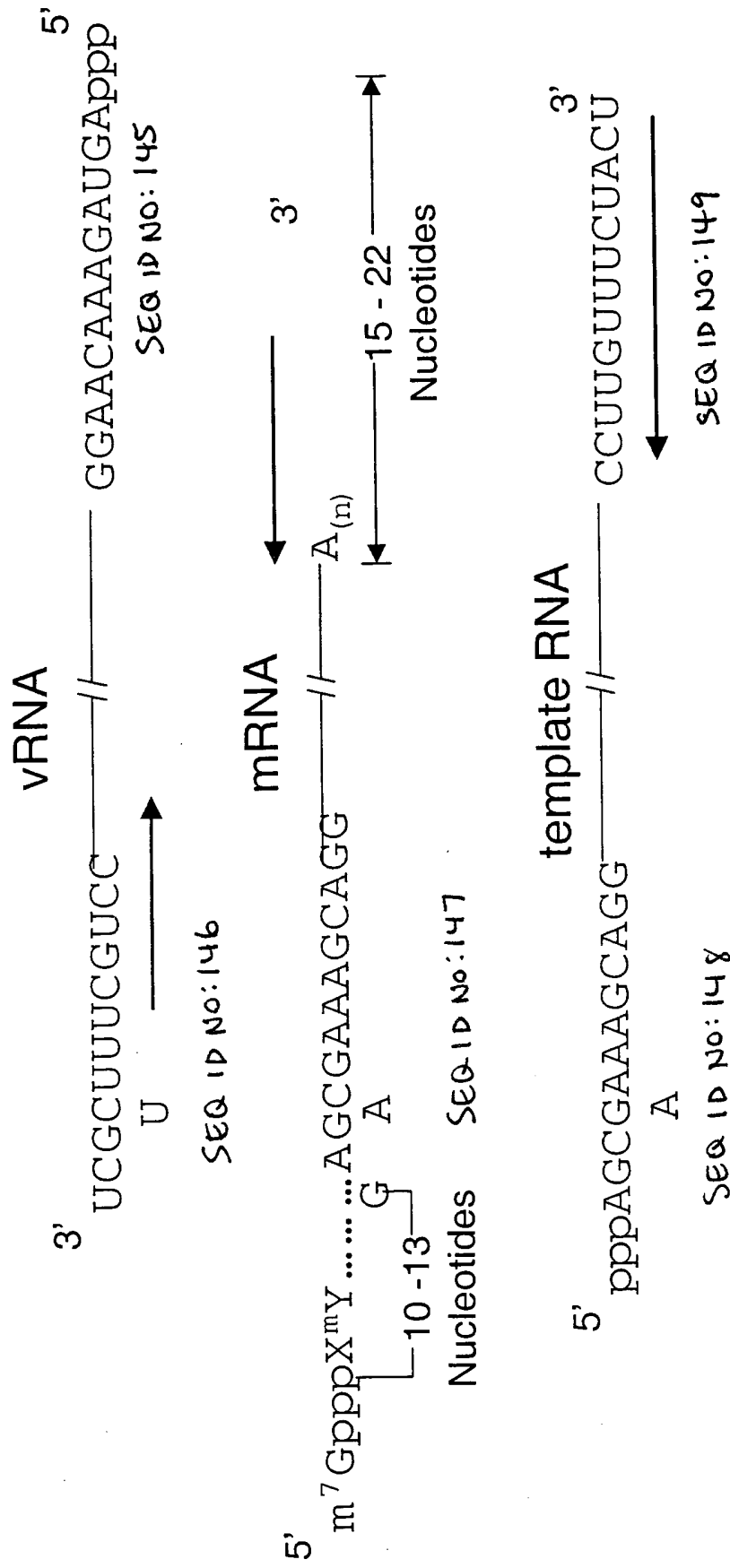


Figure 16 B

NP siRNA interferes with virus replication at a very early stage

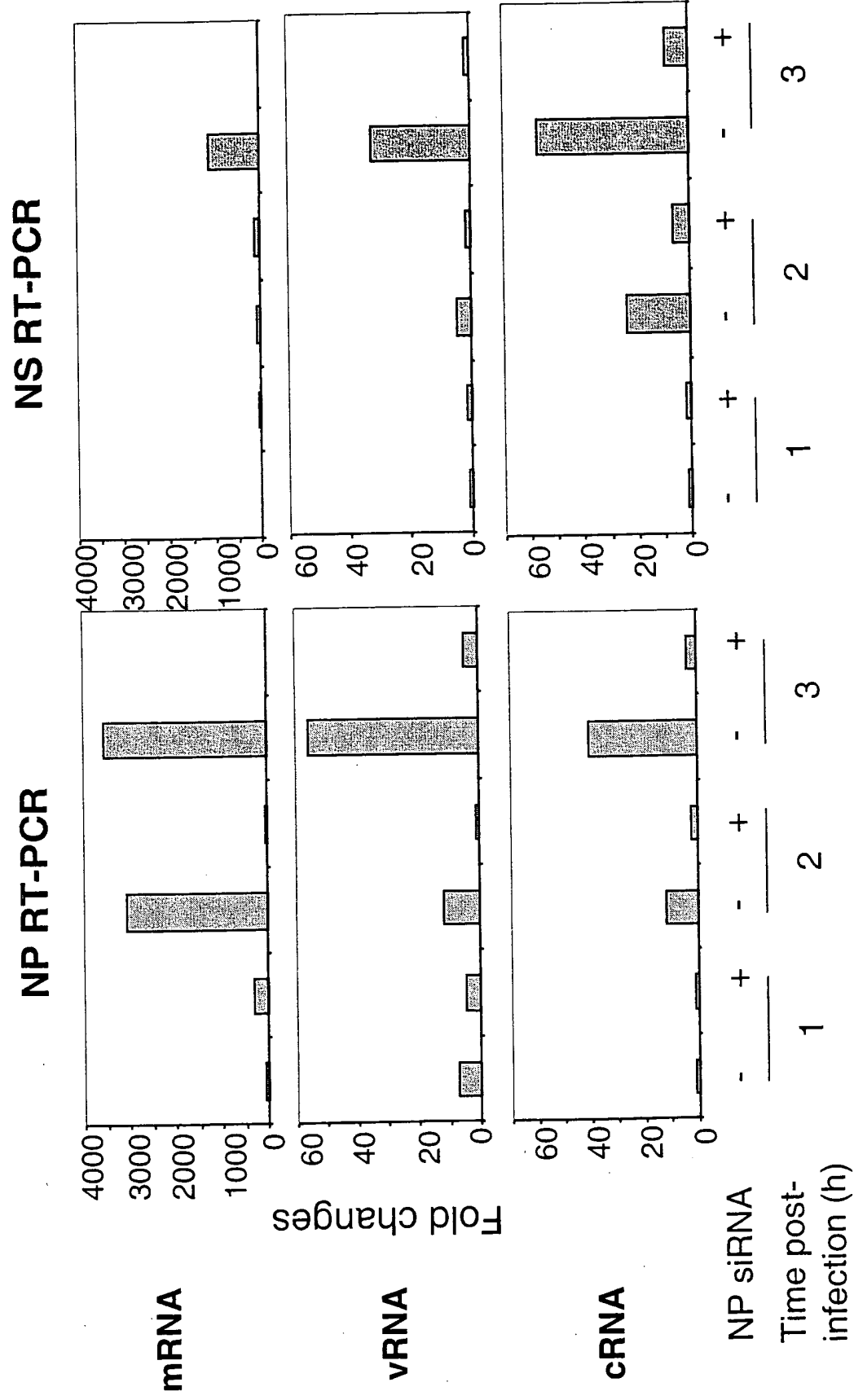


FIGURE 17

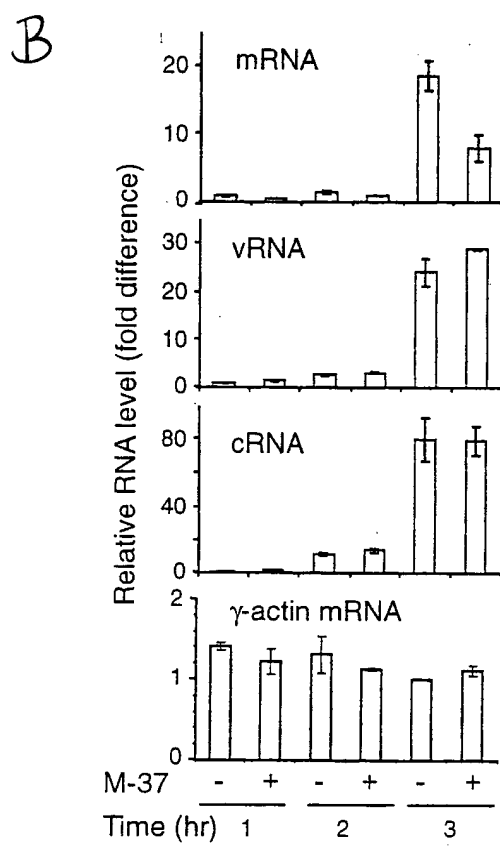
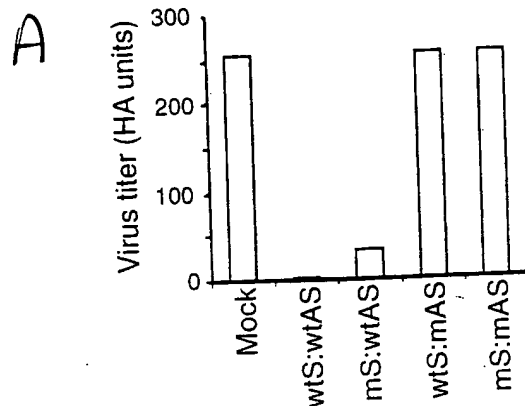


Figure 18

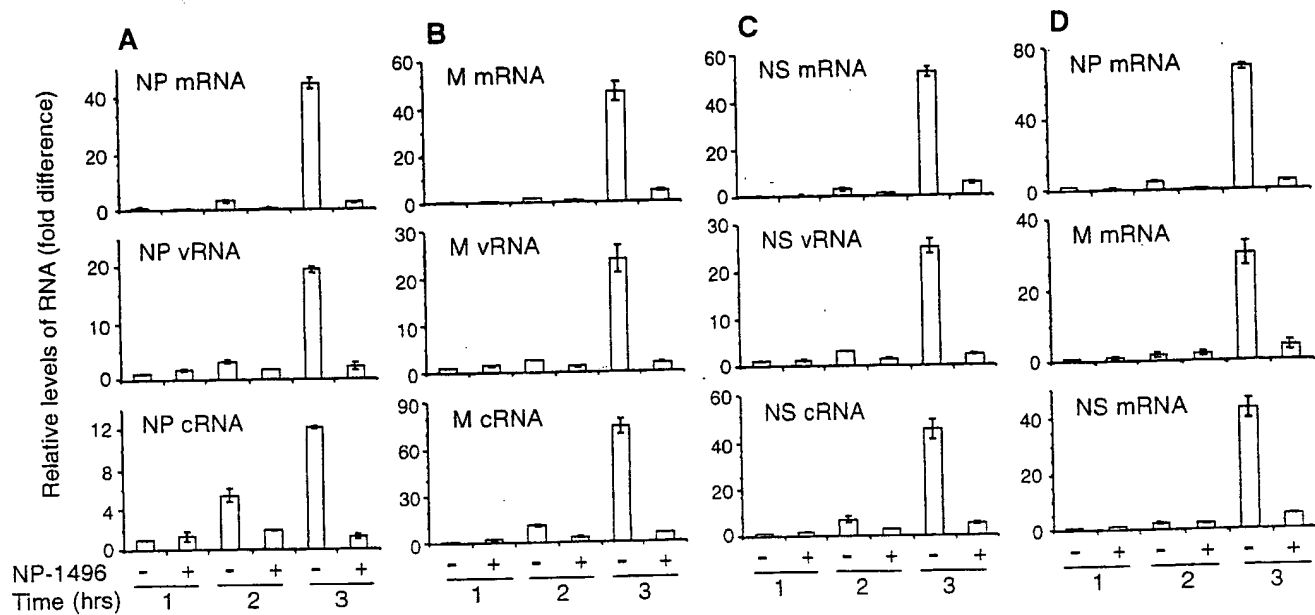


Figure 19A-D

NP and PA siRNA interferes with viral mRNA transcription

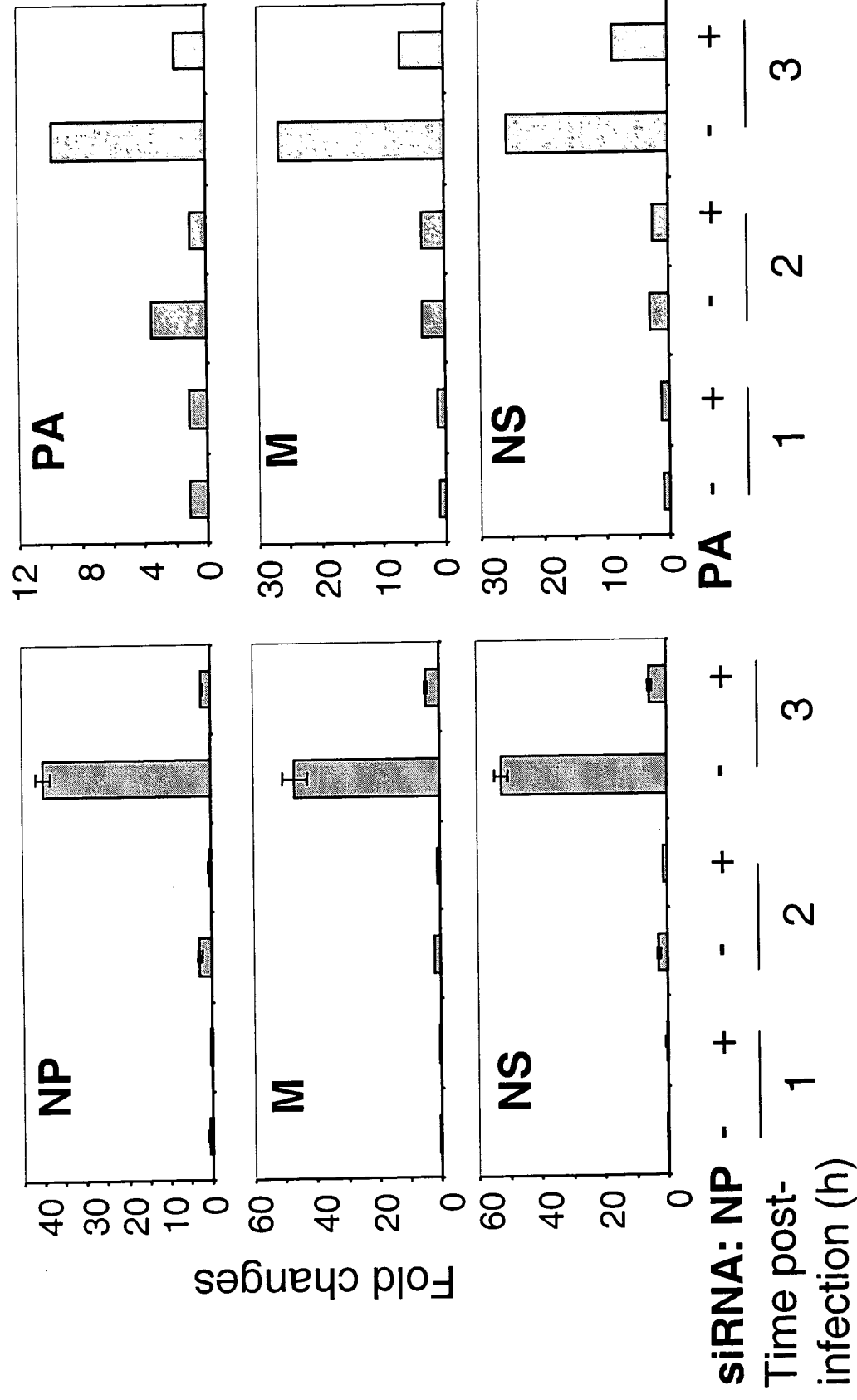


Figure 19E

NP and PA siRNA interferes with viral vRNA replication

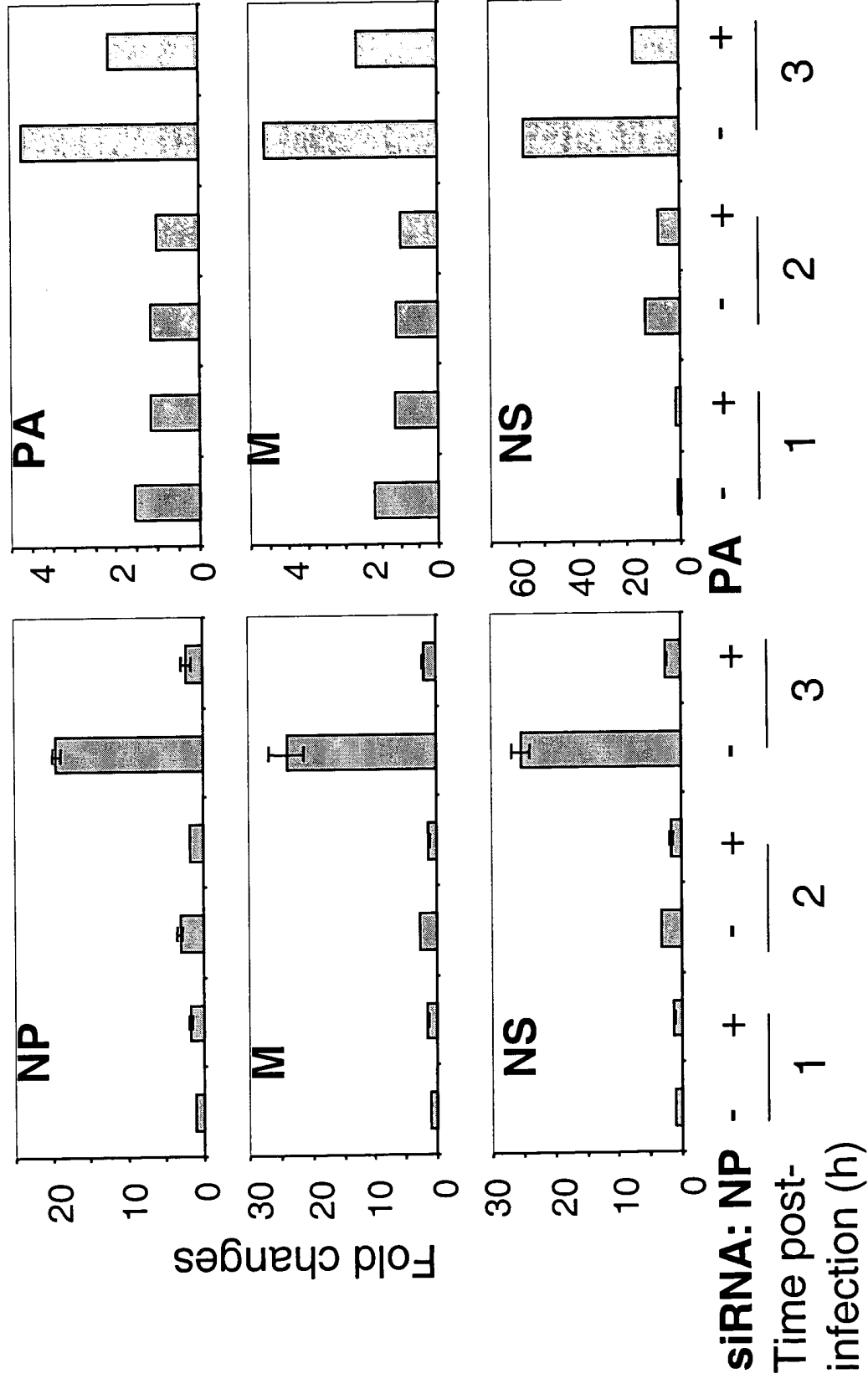


Figure 19F

NP and PA siRNA interferes with viral cRNA replication

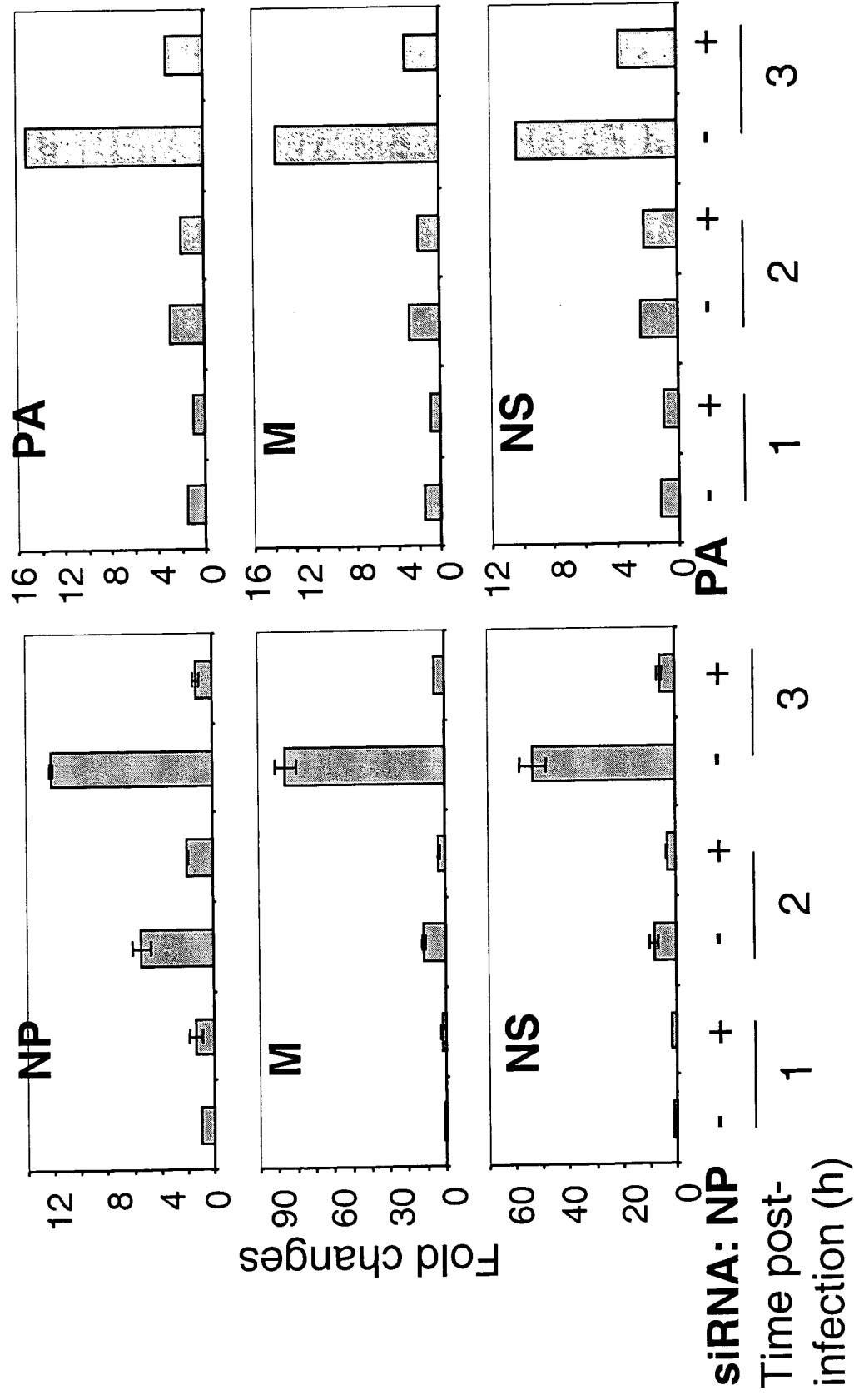


Figure 19G

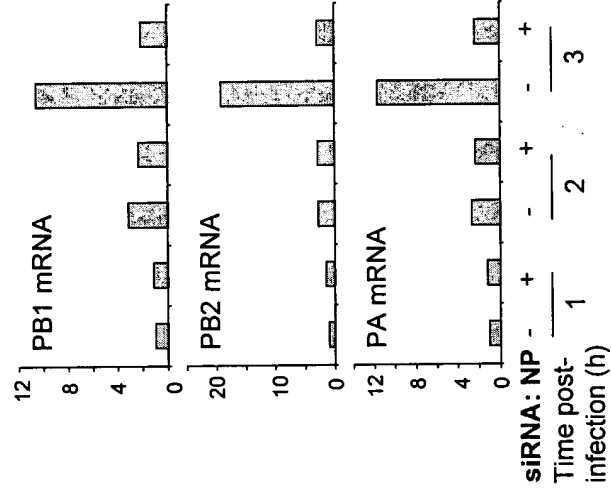


Figure 19H

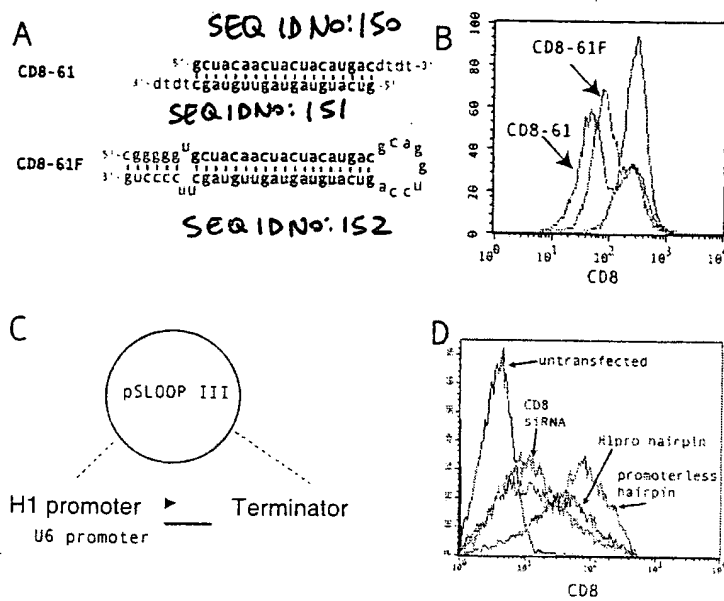


Figure 20

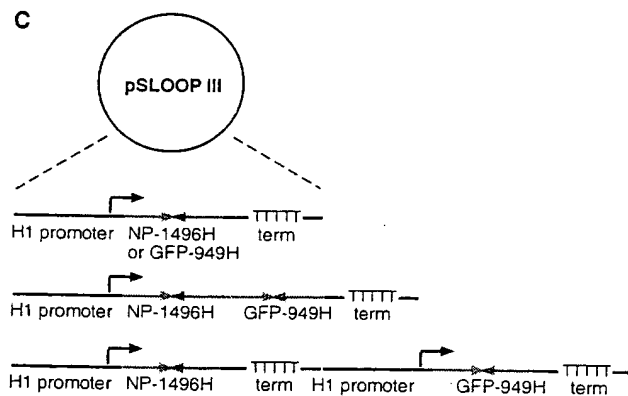
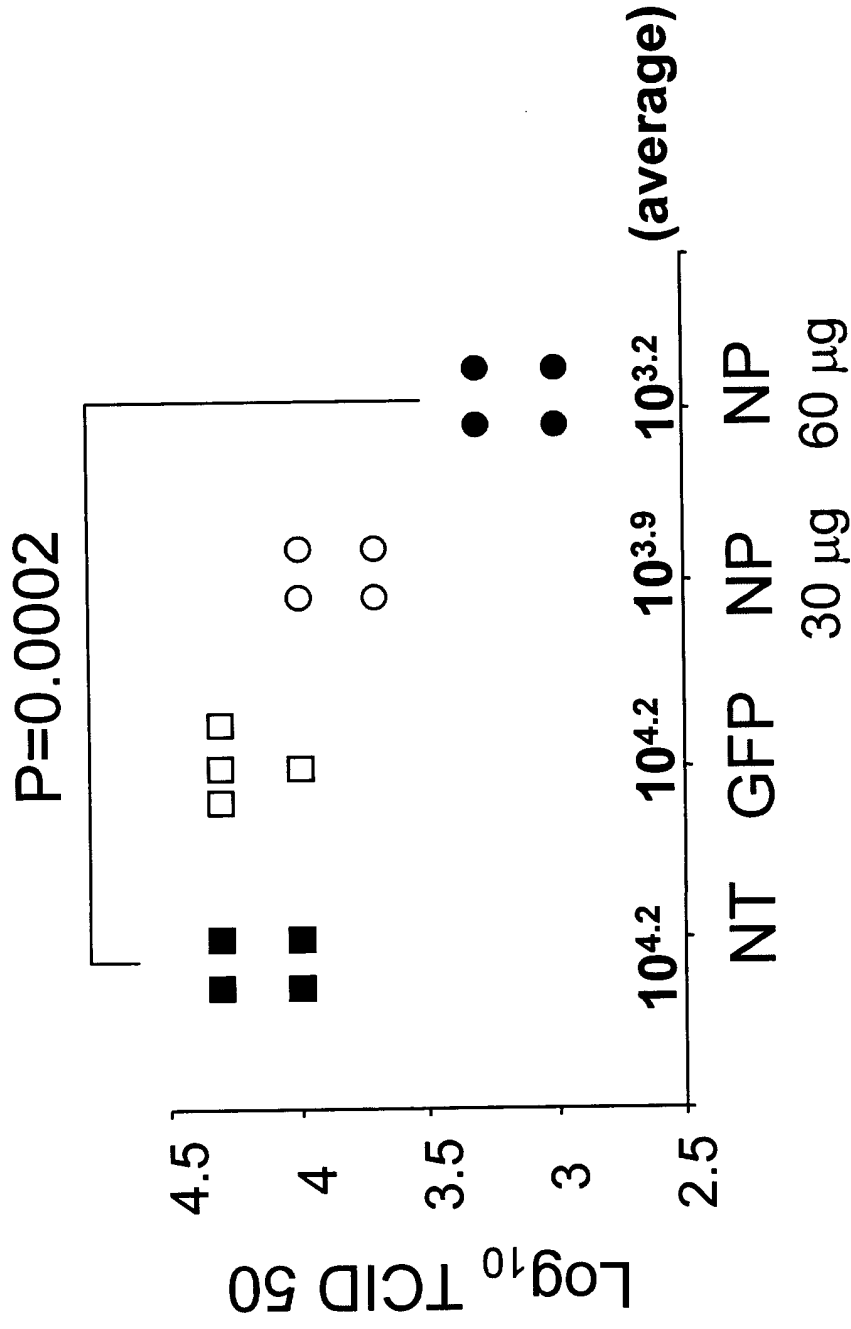
[illegible]

Figure 21

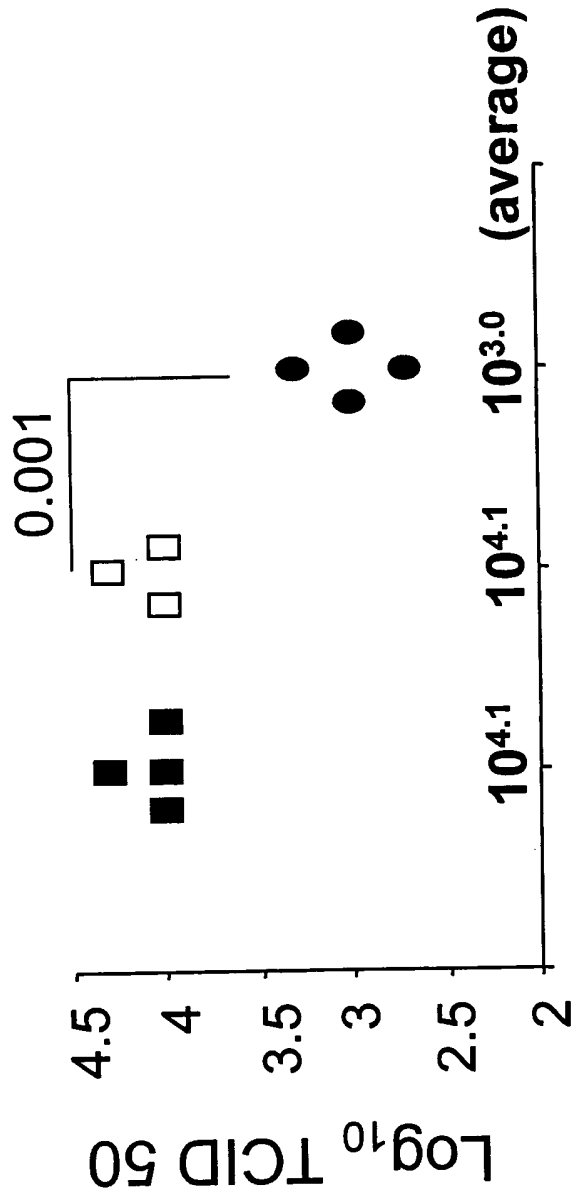
siRNA prevent influenza virus production in mice



siRNA + 3 h → PR8, 24 h → 25 μl lung → MDCK
 Carrier 1, i.v. 2k pfu/mouse homogenate HA assay

Figure 22 A

The in vivo Transfection Effect of Poly-L-Lysine(42K)

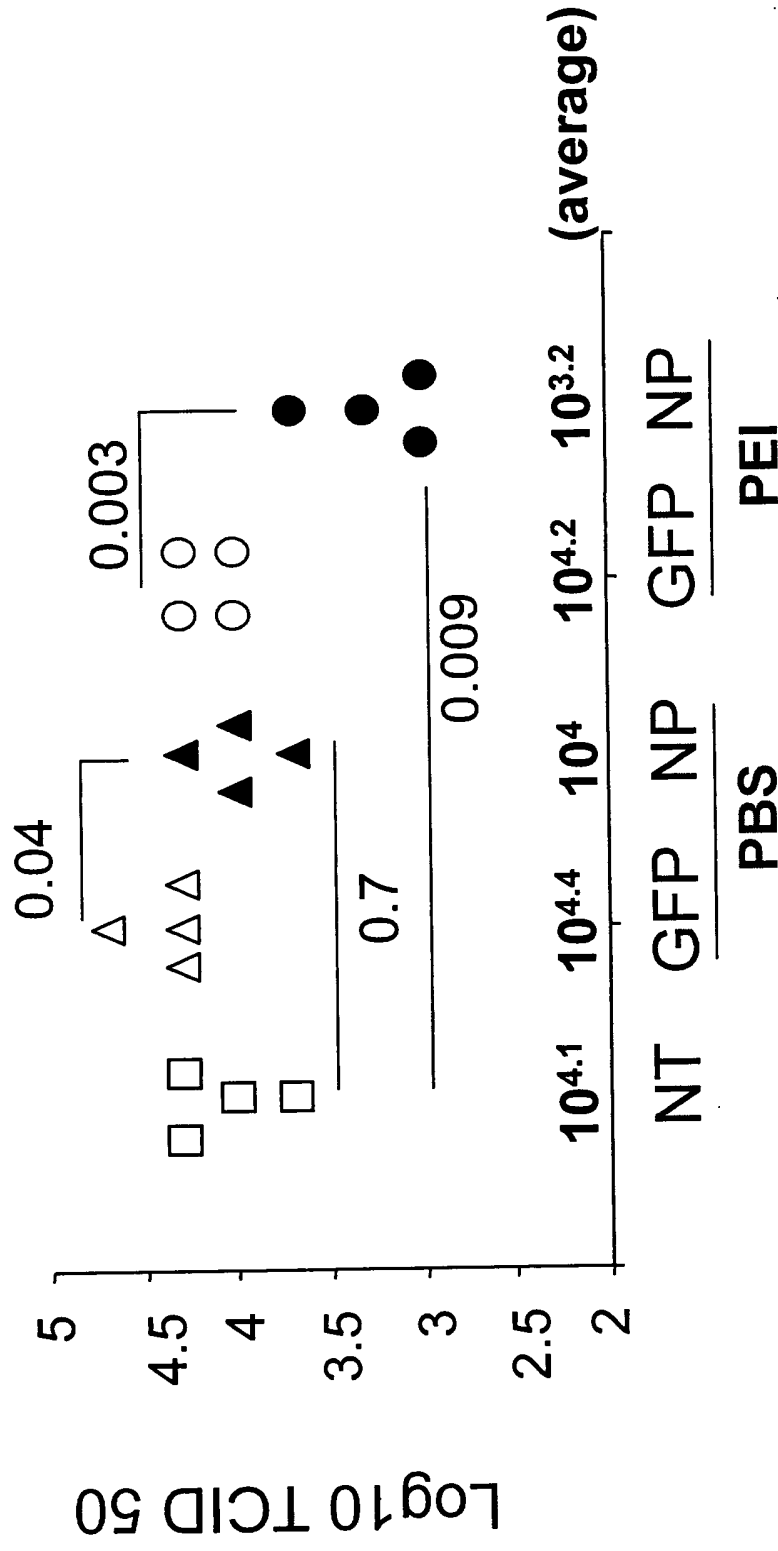


NT GFP NP
60 µg 60 µg

siRNA + 3 h → PR8, i.n. 24 h → MDCK
PLL, i.v. 12k pfu/mouse homogenate HA assay

Figure 22B

siRNA Prevent Influenza Virus Production in vivo



siRNA -/+ 3 h → PR8, i.n. 24 h → 25 µl lung → MDCK
 PEI, i.v. 12k pfu/mouse → homogenate → HA assay

Figure 22C

Additive/synergistic effect of siRNA against influenza virus in mice

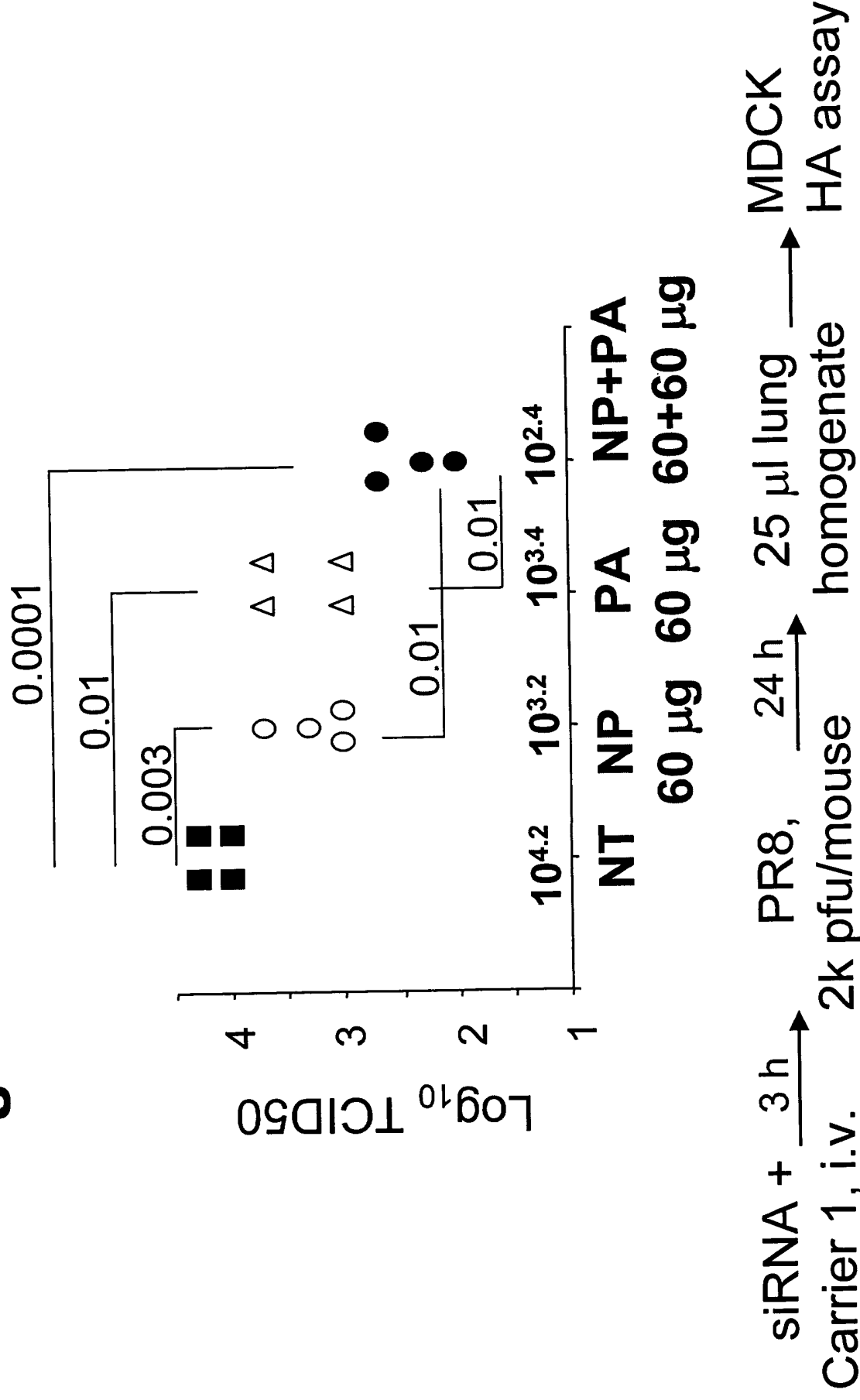


FIGURE 23

siRNA inhibit influenza virus Production in infected mouse

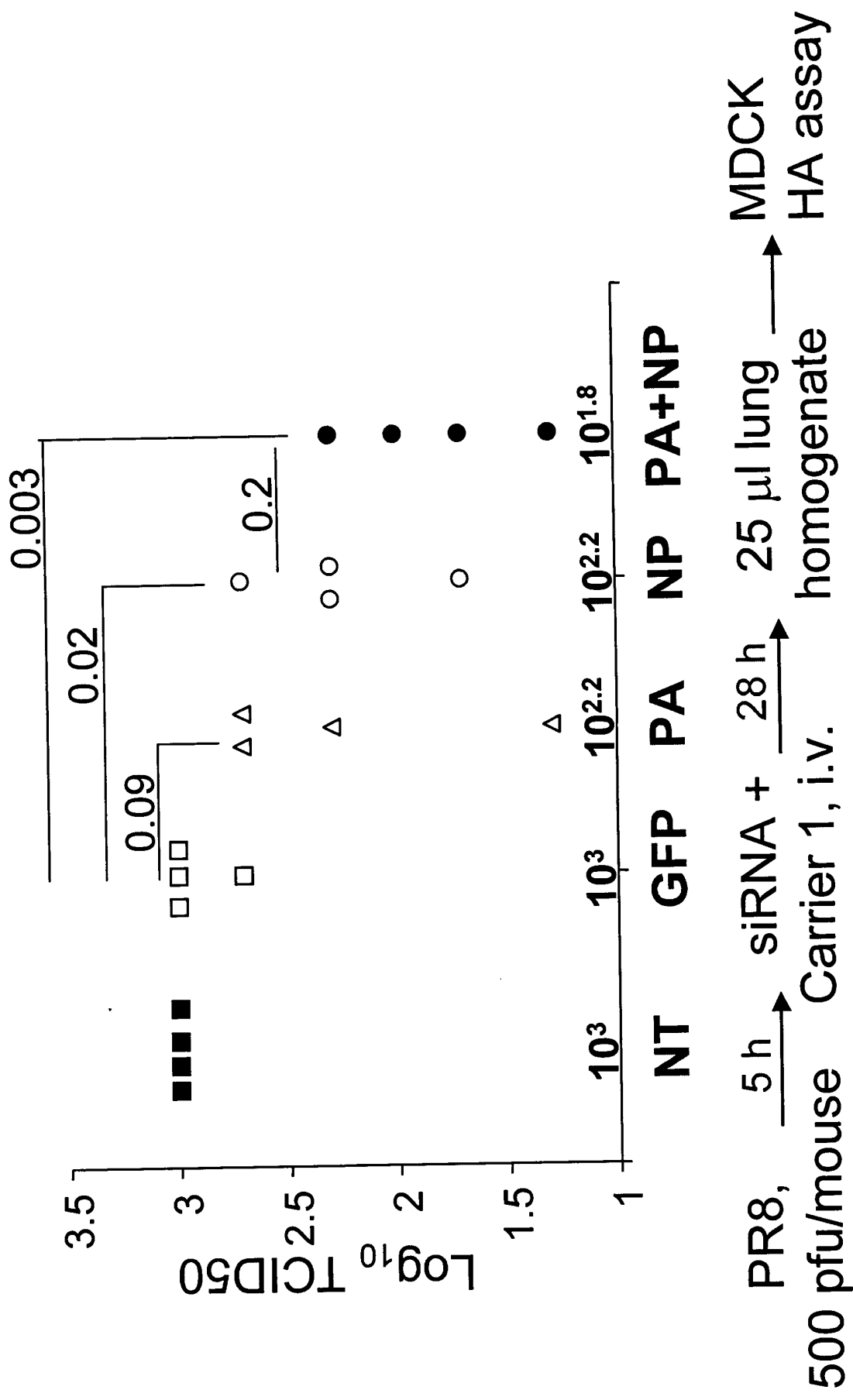


FIGURE 24

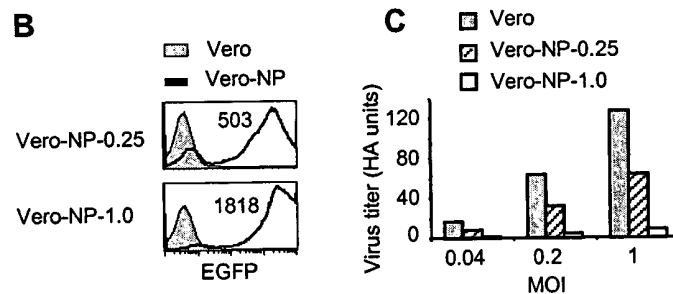
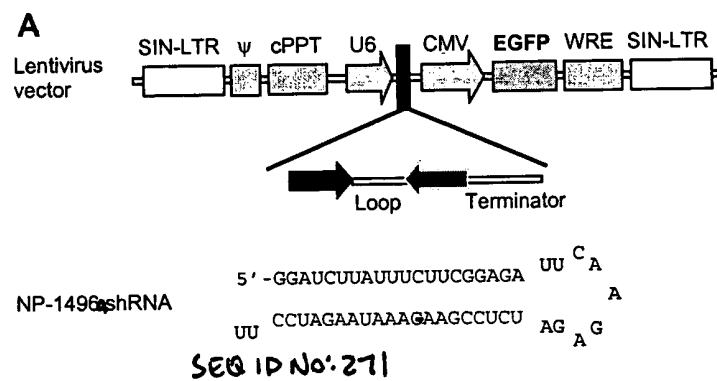


FIGURE 25

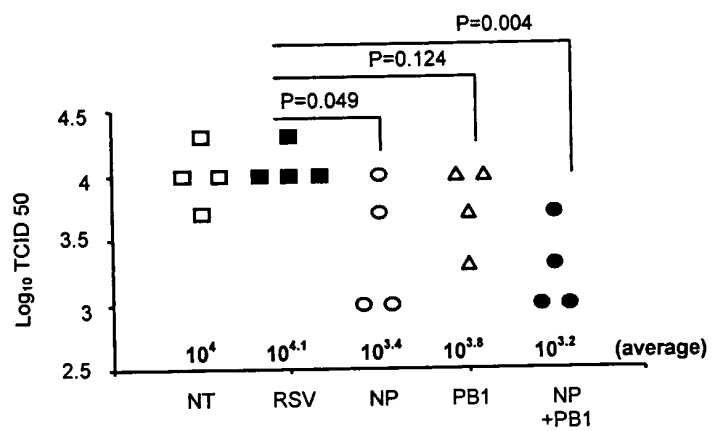


FIGURE 26

Electrophoretic retardation of siRNA with poly-L-lysine

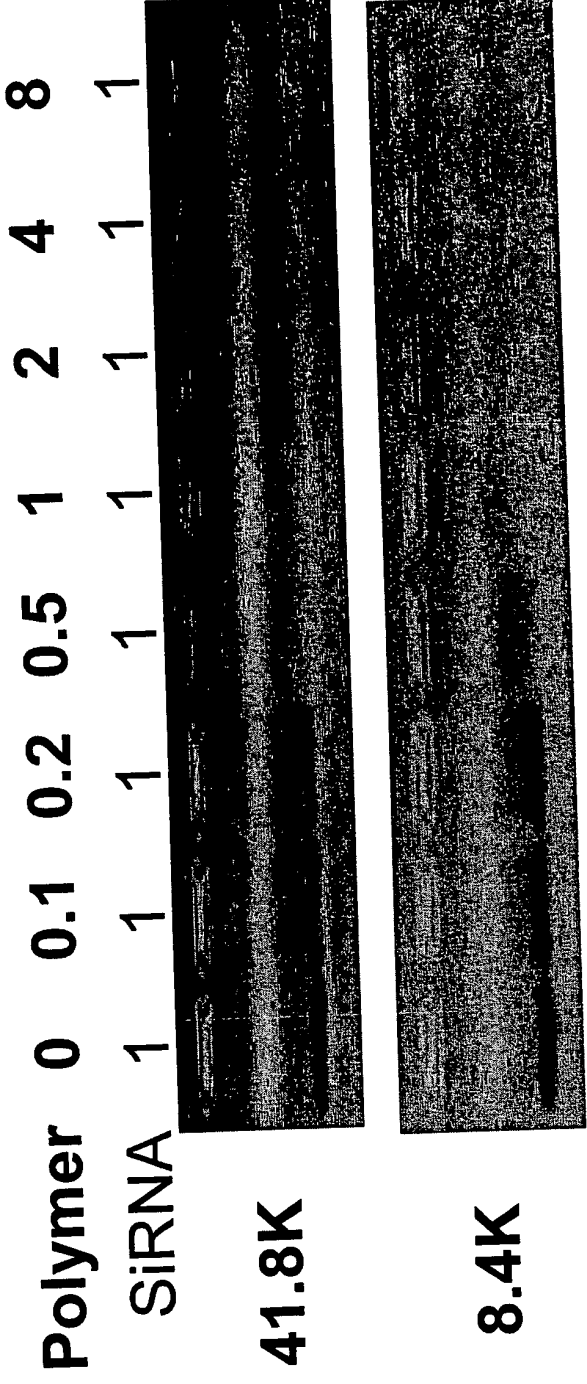


Figure 27A

Electrophoretic retardation of siRNA with poly-L-arginine

PLA	0	0.02	0.06	0.17	0.5	1.5	4.5	13.5	43.5
SiRNA	1	1	1	1	1	1	1	1	1

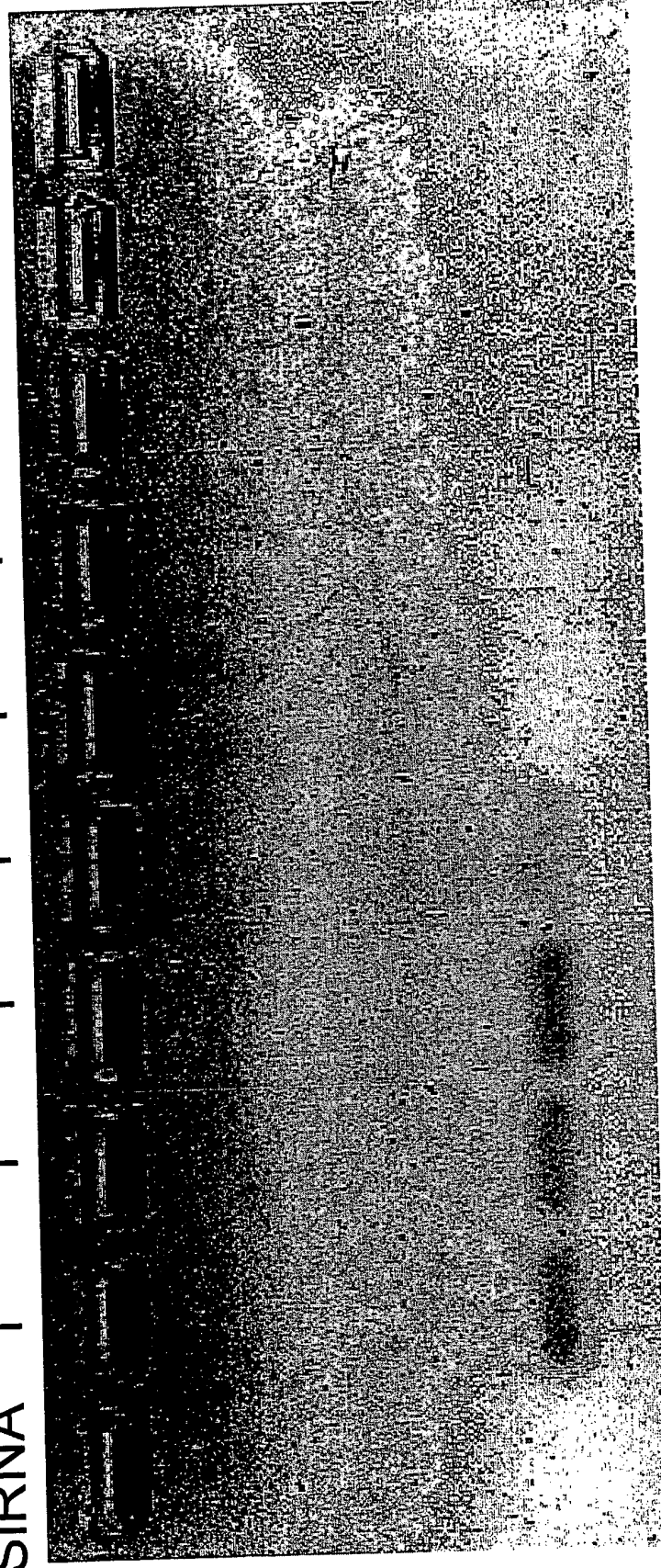


FIGURE 27B

Comparison of poly-L-lysine with different molecular weight

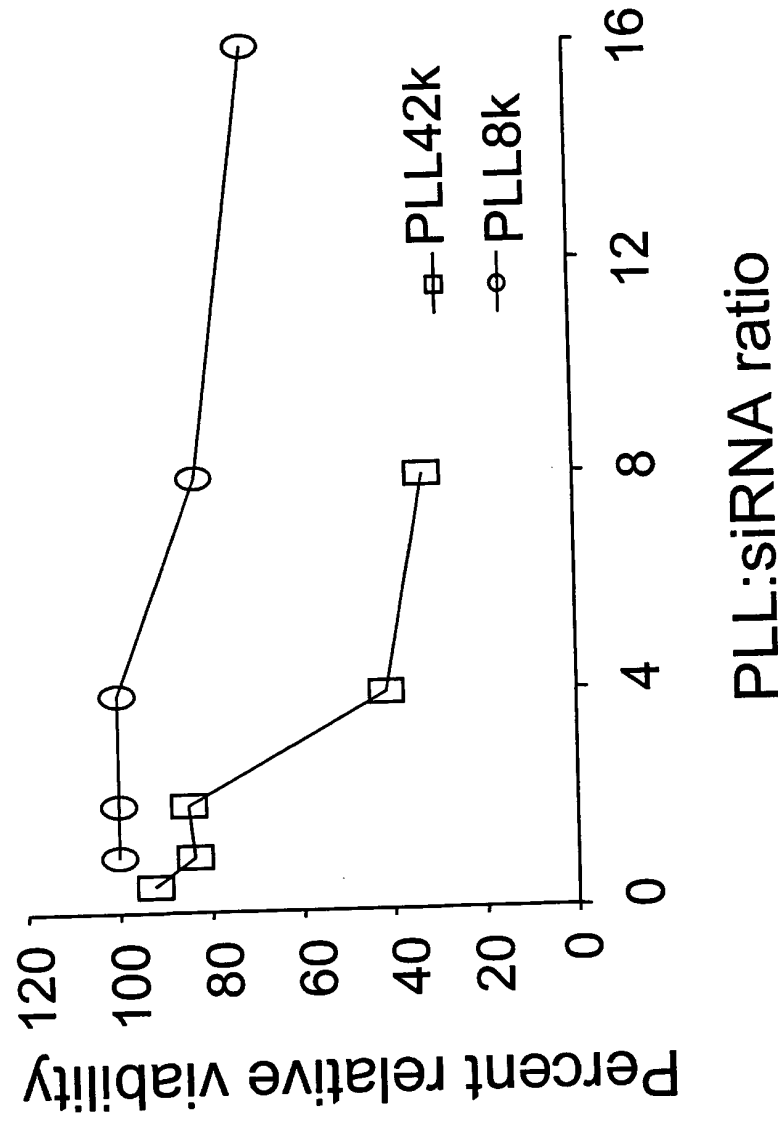


FIGURE 28A

In vitro cytotoxicity of poly-L-arginine

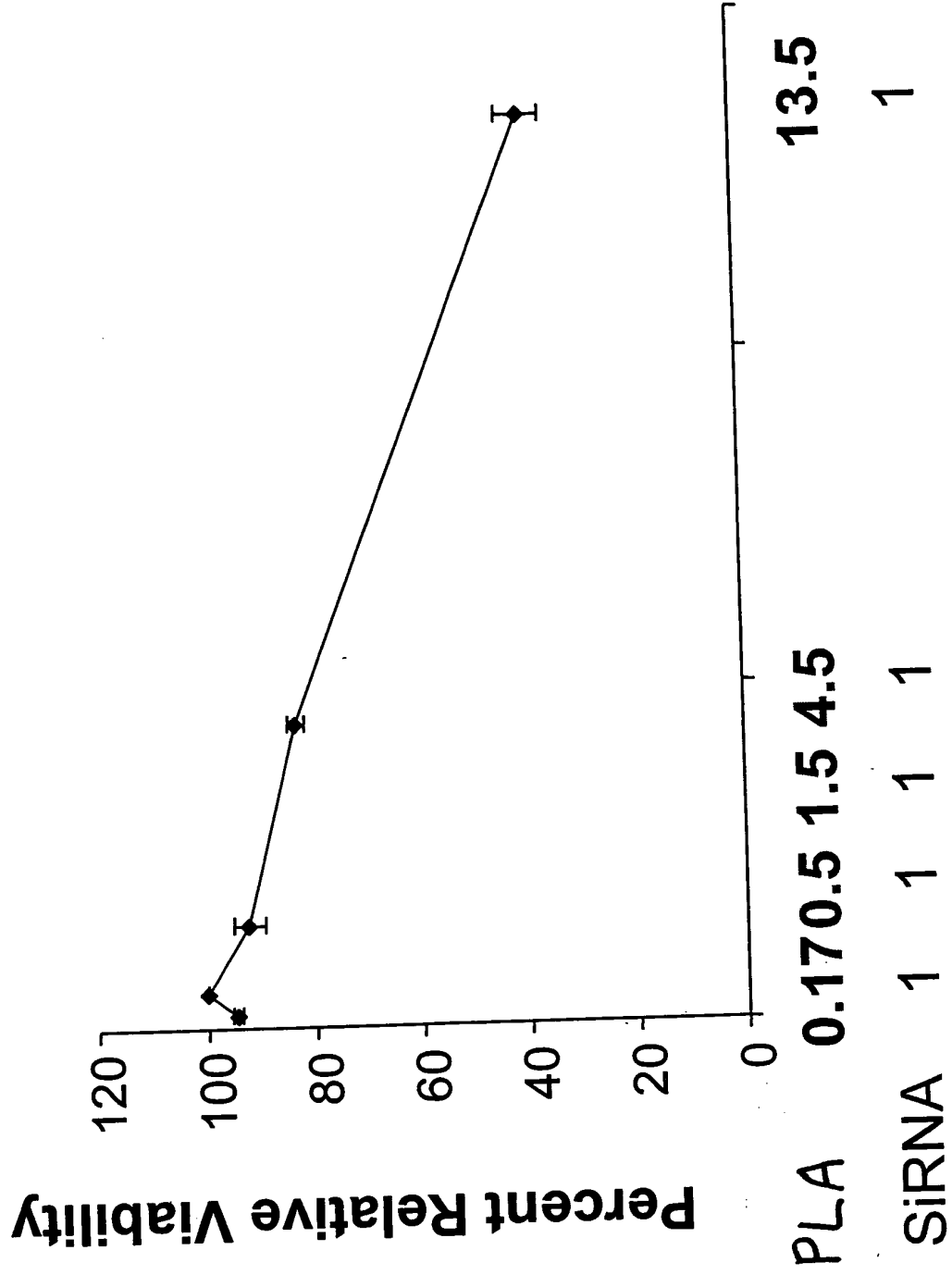
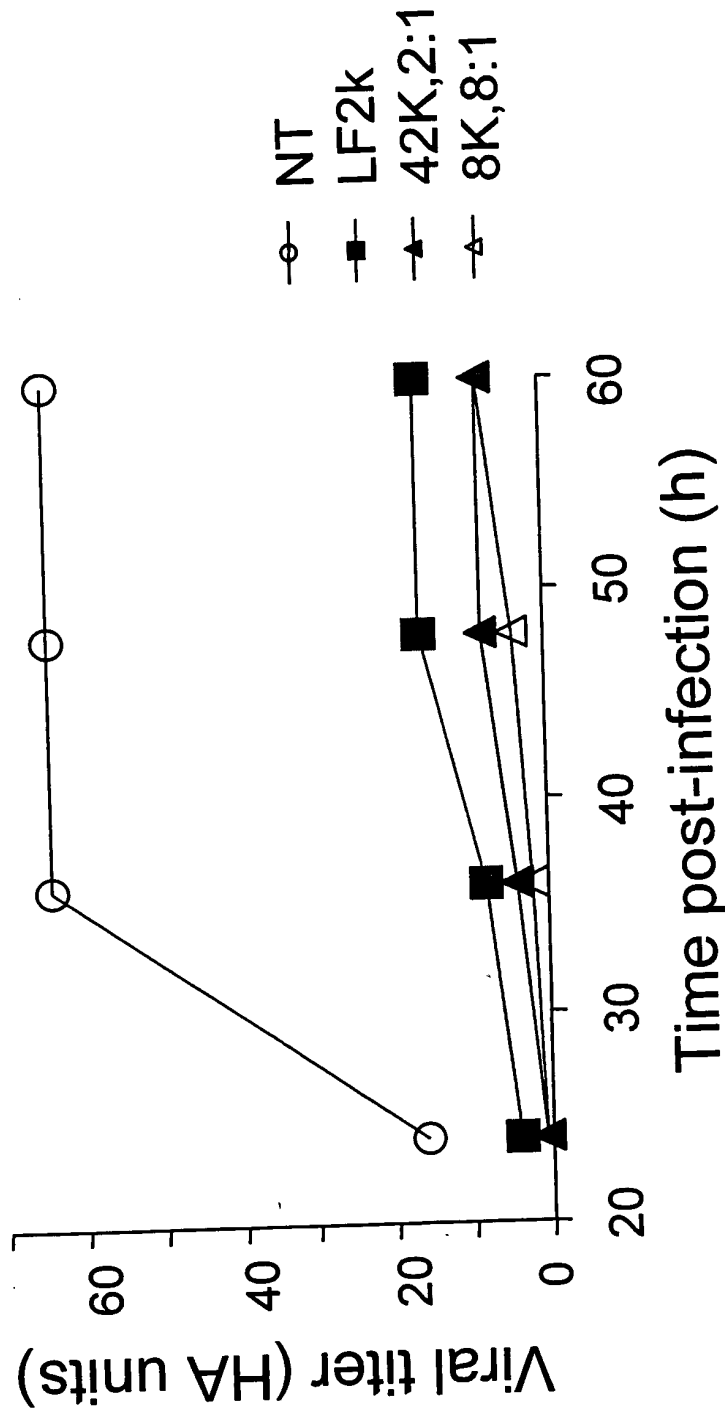


FIGURE 28B

Comparison of poly-L-lysine with different molecular weight



siRNA: 4×10^{-10} M

42K PLL: 2.9×10^{-10} M

8.4K PLL: 57×10^{-10} M

Figure 29A

Poly-L-arginine helps cellular uptake of siRNA in vitro

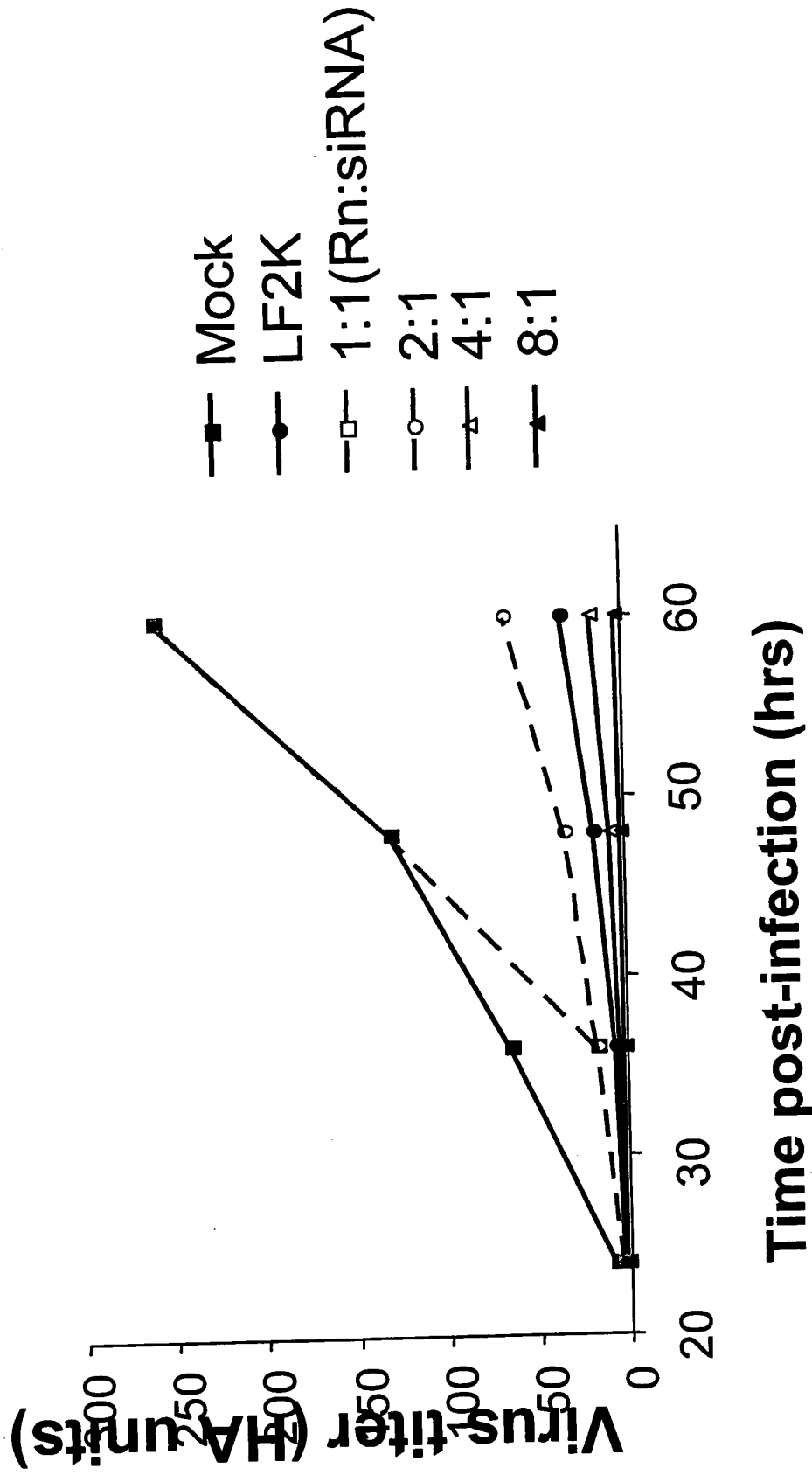


FIGURE 29B